

**FIGURE 1**

CCAATCGCCCGGTGCGGTGGTGAGGGTCTCGGGCTAGTCATGGCGTCCCCGTCTCGGAGAC  
TGCAGACTAAACCAGTCATTACTTGTTCAGAGCGTTCTGCTAATCTACACTTTTATTTTC  
TGGATCACTGGCGTTATCCTTCTTGCAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA  
CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCCTCGTGCTCATTGCTACTGGTACCG  
TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA  
AAACGTATGCAATGTTTCTGACTCTCGTTTTTTTGGTCGAACTGGTCGCTGCCATCGTAGG  
ATTTGTTTTTCAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC  
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT  
TGTGTGGTGTCACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT  
TCCTAAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA  
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA  
ATTCCTTTGGAGTTGCTTGCTGCCAACTGATTGGAATCTTCTCGCCTACTGCCWCCTCTCG  
TGCCATAACAAATAACCAAGTATGAGATAGTGTAACCCAATGTATCTGTGGGCCTATTCTCT  
CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAAGTG  
ACAACACTACTTACTGATAGACCAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT  
GTAGACCTAAAACCTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT  
TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTCTGTTAGATCG  
TTGAAACCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAAATGAAGT

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## **FIGURE 2**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGKVSLENYFSLLNEKATNVPF
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPSCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGGVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-42

#### **Transmembrane domains:**

amino acids 19-42, 61-83, 92-114, 209-230,

#### **N-glycosylation site.**

amino acids 134-138

#### **Tyrosine kinase phosphorylation site.**

amino acids 160-168, 160-169

#### **N-myristoylation site.**

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 69-80, 211-222

**FIGURE 3**

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA  
GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGCTGGGCCCGGGAGGTAGAGAAAGTCAGT  
GCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT  
TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG  
GCCGGGGTAGGCTCTGGAAAGGGCCCGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA  
GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCTAGAAAGAGGGT  
GTTCCCTCTTTGCGGGGTCTCACCAGAAGAGGTTCTTGGGGTCGCCCTTCTGAGGAGGCT  
GCGGCTAACAGGGCCAGAACTGCCATTGGATGTCCAGAATCCCTGTAGTTGATAATGTTG  
GGAATAAGCTCTGCAACTTTCTTTGGCATTGAGTTGTTAAAAACAAATAGGATGCAAATTCC  
TCAACTCCAGGTTATGAAAACAGTACTTGGAAACTGAAACTACCTAAATGATCGTCTTTG  
GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGCCAGGGTCTGTTGTTGACTCTCGAAGAG  
CACATAGCCCACTTCTTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG  
CCGAGATGACAGTGGAACAGATGACAGTGTGACACCCAAACAGCAACAGGCCGAGAACAGTG  
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTGCGCCACCAAGGAGGGGC  
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTGACACACT  
GGCAGTAATACGGACTCTTGTAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGAAT  
GAAAAGTGTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG  
CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA  
TGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGCTCTGGAATGTCTAAATGTTTC  
TGTAGCAGAAAAACAGATAAAGCTATGATCTTTATTAGAG

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## **FIGURE 4**

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ  
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKQNV DGLVLDTLAVIRTLVDKO

**Signal peptide:**

amino acids 1-16

**Casein kinase II phosphorylation site.**

amino acids 22-26, 50-54, 113-117

**N-myristoylation site.**

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

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# **FIGURE 5**

GGCACGAGGCGCTGTCCACCCGGGGGCGTGGGAGTGAGGTACCAGATTAGCCCATTTGGCC  
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCCTAACGGACTG  
CAAG**GATG**GAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT  
CAGGTGCCTGGGGCATGCAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC  
CTTCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTTCCCTTCTACTTCCACATCTC  
CATGGGCTGTGCC TTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA  
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCTCTGAGCCTTACGCTGGCCACTGTCAAC  
GCCCCTGGCTGGAACCCCGCACACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA  
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC  
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTTCCGCTACCATGGGCTGTCC  
TCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA  
AATAAGGAGCCT**CTAG**CATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAA  
AAAAAAAAAAAA

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## **FIGURE 6**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGGNLGGLIKMHVHLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPPYFHISM  
GCAFINLCILASQHAWAQLTFWEASQLYLLFLSLTLATVNNARWLEPRTTAAAMWALQTVEKER  
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFFRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

### **Signal peptide:**

amino acids 1-24

### **Transmembrane domain:**

amino acids 86-103, 60-75

### **Casein kinase II phosphorylation site.**

amino acids 82-86

### **Tyrosine kinase phosphorylation site.**

amino acids 144-151

### **N-myristoylation site.**

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 54-65

### **G-protein coupled receptors proteins.**

amino acids 44-85

**FIGURE 7**

AATTCAGATTTTAAAGCCATTCTGCAGTGGAAATTCATGAAGTAGCAAGAGGACACCATCTT  
 CTTGTATTATACAAGAAAGGAGTGACCTATCACACACAGGGGAAAAATGCTCTTTTGGGT  
 GCTAGGCCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAACTAAAGATTGAAG  
 ACATCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCC  
 AGAACTTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC  
 AGCTTTAAAGGCAGAACTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG  
 AGAATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGT  
 CTGATCAATAATGCTGGTGTCCCGGCGTGTGGCTCCCACTGACTGGCTGACACTAGAGGA  
 CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC  
 CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTTGGAGGTCGCCCTTGCA  
 ATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGGAAAGTTTCAATGACAGCTTAAG  
 ACGGGACATGAAAGCTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAA  
 ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAACTCGCCATTGGGGAGCAGCTGTCTCCA  
 GACATCAAAACAACATATGGAGAAGGTTACATTGAAAAAGTCTAGACAACTGAAAGGCAA  
 TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA  
 GTCTCTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAATTTCTGGATACTCTG  
 TCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA  
 TCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT  
 TTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTTAGA  
 TCGTGCTTATTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCAGGGTCCCTG  
 CTCAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCTGCCCTGT  
 ATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAATTGAAAGACTTGCCCATTCAAATG  
 ATCTTTACCGTGGCCTGCCCATGCTTATGGTCCCAGCATTTACAGTAACTGTGGAATGTT  
 AAGTATCATCTCTTATCTAAATATTAAAGATAAGTCAACCCAAAAA  
 AAAAAAAAAAAAAAAAAA

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## **FIGURE 8**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406
><subunit 1 of 1, 319 aa, 1 stop
><MW: 35227, pI: 8.97, NX(S/T): 3
MLFWVLGLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGPHVIAACLT
ESGSTALKAETSERLRVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDW
LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSIEPGLFKTNLADPVKVIKKLAIWEQLSPDIKQQYGEGYIEKSLD
KLKGNKSYVNMDLSPVVECDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLKQK
AELANPKAV
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-17

#### **Transmembrane domain:**

amino acids 136-152

#### **N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

#### **Glycosaminoglycan attachment site.**

amino acids 39-42

#### **N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212



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**FIGURE 9**

GCGGGCTGTTGACGGCGCTGCG**ATGG**CTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT  
 CCTCTCAGTCGGACTTCTCTGACGCCGCCAGTGGGCGGGGCCCCCTTGGGGCCGTGCGCCACCCT  
 GTAGTCATGTACCCACCGCCGCCGCCGCCCTCATCGGGACTTCATCTCGGTGACGCTGAG  
 CTTTGGCGAGAGCTATGACAAAGCAAGAGTTGGCGGCGCGCTCGTGCTGGAGGAAATGGA  
 AGCAACTGTCCGAGATTGACGCGGAATATGATTCTCTTCTCCTTGCCTTTCTGCTTTTCTGT  
 GGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTTCAGGCTAGAGGA  
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTAAAAACCAGCAAAATCCACCCGCTCTTACCAG  
 CTCTCTCAGAAGGCGGACACCGACCCTGAGAACTTACCTGAGATTTCGTCACAGAAGACACAA  
 AGACACATCCAGCGGGGACCACCTCACCTGCAGATTAGACCCCAAGCCCAAGACCTGAAGGA  
 TGGGACCCAGGAGGAGGCCACAAAAAGGCAAGAAGCCCCGTGGATCCCCGCCCGGAAGGAG  
 ATCCGCGAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGGCACCAG  
 CTCCCTTCAAGAAGAGCAGAAGTGCCACCAAGCCTCCCTGCCACCGGCCAGGACACAGGG  
 CACACCAGTGCATCTGAACATATCGCCAGAAGGGCGTGATTGACGCTTCTCCTGCATGCATGGA  
 AAGGATACCCGAAGTTTGCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCCTTCAGT  
 GAGTGGTTTGGCCCTCGGTCTCACACTGATCGACGCGCTGGACACCATTGGATCTTGGGTCT  
 GAGGAAGAATTTGAGGAAGCCAGGAAGTGGGTGTGCAAGAAGTTACACTTTGAAAGGACG  
 TGGACGTCAACCTGTTTGAAGACACGATCCGCATCCTGGGGGGCTCCTGAGTCCCTTACCAC  
 CTGTCTGGGGGACAGCCTTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGGCTAATGCCCTGC  
 TCTCAGAACACCATCCAAGATTCTTCTACTCGGATGTGAACATCGGTACGTTGGAGTTGCCACC  
 CGGCCAGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTAGCTGGAGTTCGGG  
 GAGTCTCCTGCTCACAGGGGATAAGAAGTTTCAGGAGGCAGTGGAGAAGGTGACACAGCA  
 CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTCATCAATACCCACAGTG  
 GCCTCTTACCCACCTGGGCGTATTACAGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC  
 CTGTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGGATGGAAGACTACGTGGGA  
 AGCCATCGAGGGTGTGAGAAGCACTGTCTGCGGCACTCCGAGCCAGTAAGTCACTTTG  
 TGGGGGAGCTTGCCACGGGCCCTTCAGTGCCAAGATGGACCACCTGGTGTGCTTCTGCCA  
 GGGACGCTGGCTCTGGGCGTCTACCACGGCCTGCCCGCCAGCCACATGGAGCTGGCCCCAGGA  
 GCTCATGGAGACTTGTTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCAGAGATCG  
 TGCATTCAACCTTTACCCCGAGCGGGCCGTGCGGACGTGGAGGTCAAGCCAGCAGACAGG  
 CACAACCTGTCTGGCCAGAGACCGTGGAGAGCCTGTTCTACCTGTACCGCGCTCACAGGGGA  
 CCGCAAAATACAGGACTGGGCGTGGGAGATTCTGCAGAGCTTCAGCCGATTACACGGGTCC  
 CCTCGGGTGGCTATTCTTCCATCAACATGTCCAGGATCTCAGAAGCCCGAGACCGTAAAGGAC  
 AAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTGCTCTTCTCCGATGA  
 CCCAAACCTGCTCAGCCTGGACGCCATCGTGTTCACACCCAGGCCACCTCTGCTCTATCT  
 GGACCCCTGCG**TAGGG**TGGATGGTGTCTGGTGTGGGGACTTCGGGTGGGCAGAGGCACCTTG  
 CTGGGTCTGTGGCATTTTCCAAGGGCCACGTAGCACCGGCAACCGCCAAGTGGCCCCAGGCT  
 CTGAACCTGCTTGGGCTCCTTCTCGTCTCTGCTTAATCAGGCTGAGGACCAAGTGA  
 GGCGCTCAGTCTTGGTGTGATGCGGGGTGGGCTGGGCGCTGGAGCCTCCGCTGCTTCTCT  
 CAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGCTCTGTGGGCCGACCA  
 GAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGGACAGCCAGGGTGCAGC  
 TCTGCCCGGCTCGTGAAGCCTCAGATGTCCCCAATCCAAGGGTCTGGAGGGGCTGCCGTGA  
 CTCGAGAGGCTGAGGCTCCAGGCTGGCTCTGGTGTTCAGAAGCTGGACTCAGGATCCTC  
 CTGGCCGCCCGCAGGGGGCTTGGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGGCCCT  
 CCAGTGAATGGGTCTTTTCGGTGGAGATAAAGATTGATTTGCTCTAACCGCAA

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**FIGURE 10**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529
><subunit 1 of 1, 699 aa, 1 stop
><MW: 79553, pI: 7.83, NX(S/T): 0
MAACEGRRSGALGSSQSDFLTTPVGGAPWAVATTVMYPPPPPPPHRDFISVTLSFGESYDN
SKSWRRRSCWRKWKQLSRLQRNMILFLAFLFCGLLFYINLADHWKALAFRLEEEQKMRPE
IAGLKPANPPVLPAPOKADTDENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTEQEEAT
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTLPSSRAEVPTKPPLPPARTQGTPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEKDVDVNLFESTITRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSDEVNIGTGVAHPPRWTSDSTVAEVTISIQLFRELSSRLTGDKKFQEAWEKVQHIHLSGK
KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWIQGGKQETQLEDYVEAIEGVRT
HLLRHSEPSKLTFFVGEAHGRFSKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLRLPETVESLFYLYRVGTDRKYQDWG
WEILQSFSRFRTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETILKYLFLFSDDPNLLSLD
AYVFNTEAHPLPIWTPA

```

**Important features of the protein:****Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

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**FIGURE 11**

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCCATGCGCCGC  
 CGCCTCTCCGCACGATGTTCCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC  
 AGGTCCGGGTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTCTGTGGC  
 CTGCCTCTCGTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGTGCTCTGGGGACGTGG  
 CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCGTGCTGCCCCCAGAG  
 CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCTGGCAGTGCTGGT  
 GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCTCTGA  
 GCAGGAAGAAGATCCGGCACCACATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC  
 CGGGCAGCGCTCATCAACGTGGGCTTCTTGGAGAGCAGCAACAGCACGGACTACATTGCCAT  
 GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC  
 CCTTCCACGTGGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTCGGCGGC  
 ATCTGTGTCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG  
 CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAAGGGAGCTGGGCTCCAGCTTTTCC  
 GCCCCTCGGGAATCACAACTGGGTACAAGACATTTTCGCCACCTGCATGACCCAGCCTGGCGG  
 AAGAGGGACCAGAAGCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG  
 AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGCGGGGCCC  
 CCTGCACTGTCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTC  
 AGCTGAGCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA  
 CAAGGCCTCAGGTCTGTTGGGCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA  
 AGCTACGCAATTGCAGCCACCCGGCCGCCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG  
 GTGCCTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCTGTCCG  
 GGACCCCCCTGCCTTCTGCTCACCTACTCTGACCTCCTTCACGTGCCAGGCCTGTGGG  
 TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCTACTCTGACCTCCTTCACGTGCC  
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 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 12**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531  
><subunit 1 of 1, 327 aa, 1 stop  
><MW: 37406, pI: 9.30, NX(S/T): 1  
MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSLGFFSLLWLQLSCSGDVARAVR  
GQGQETSGPPRACFPPEPPPEHWEEDASWGPHRLAVLVPPFRERFEELLVFVPHMRRFLSRKKI  
RHHIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFFEAGPFHVA  
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDDEFYRRIKGAGLQLFRPSGI  
TTGYKTFRHLHDPAWRRDQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL  
NIMLDCDKTATPWCTFS

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 29-49 (type II)

**N-glycosylation site.**

amino acids 154-158

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 27-31

**Tyrosine kinase phosphorylation site.**

amino acids 226-233

**N-myristoylation site.**

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

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# **FIGURE 13**

CAATGTTTGCCTATCCACCTCCCCCAAGCCCCTTTACCT**ATG**CTGCTGCTAACGCTGCTGCT  
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCT  
CTTCTGCCACTGACGCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTC  
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT  
GGGGGATGGC**TAA**GAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG  
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC  
CCTGTTTCATTAAGAAATTGTTCCCTTCCCTGTGTTCATGTTTGTAAGATTGTTCTGTGT  
AAATATGTCTTTATAATAAACAGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 14**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862

<subunit 1 of 1, 73 aa, 1 stop

<MW: 7879, pI: 7.21, NX(S/T): 0

MLLLTLLLLLLLLKGSCLWGLVGAQKVSSATDAPIRDWAFPPSFLCLLPHRPAMTCSQAQ  
PRGEGEKVGDG

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

**FIGURE 15**

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAG  
 GAGCATGTCCCGGCCGGGGAAGGCCCGTCCCTCCGGCCGCCATAAGGCTCCGGTCGCCGCTGG  
 GCCCGCGCCGCGCTCCTGCCCGCCGGGCTCCGGGCGGCCCTAGGCCAGTGCGCCGCCG  
 CTCGCCCCGACAGGCCCGGCCCGCAGC**ATGG**AGGCCACCCGACGCCGCGGGGCCGCGCGCA  
 GCCGCCGCTGTTTCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCCGCGCGG  
 GCGCGCGCGCGCGCGCTGCCCGCCGGCTGCAAGCACGATGGCGGCCCGAGGGGCTGGC  
 AGGCGGCCGCGGCCCGCCGAGGGCAAGGTGGTGTGCAGCAGCCTGGAACCTCGCGCAGGTCTCT  
 GCCCCAGATACTCTGCCCAACCGCACGGTCACCTGATTCTGAGTAACAATAAGATATCCG  
 AGCTGAAGAATGGCTCATTTTCTGGGTAAAGTCTCCTTGAAAGATTGGACCTCCGAAACAAT  
 CTTATTAGTAGTATAGATCCAGGTGCCCTTCGGGGACTGTCATCTCTAAAAAGATTGGATCT  
 GACAAACAATCGAATAGGATGTCGAATGCAGACATATTTTCGAGGACTACCAATCTGGTTC  
 GGCTAAACCTTTTCGGGAATTTGTTTTCTTCATTATCTCAAGGAACCTTTGATTATCTTGGC  
 TCATTACGGTCTTTGGAATTCAGACTGAGTATCTTTTGTGTGACTGTAACATACTGTGGAT  
 GCATCGCTGGGTAAAGGAGAAGAACATCACGGTACGGGATACCAGGTGTGTTTATCCTAAGT  
 CACTGCAAGCCCCAACAGTACAGGCGGTGAAGCAGGAGCTGTTGACATGCGACCCCTCCGCTT  
 GAATTCGCGTCTTTCTACACTCCATCTCATCGCCAAGTTGTGTTGAAGGACAGCCT  
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 GGAGAATAGTTGAACCCGATGAATCGCAAGGTATTTTGTGTGAAAGAAACATGATTCACAAC  
 TGCTCCTTGATGTCAGGTGCCCTAACCATTTCTAATATTCAAGCTGGATCTACTGGAATTTG  
 GGGCTGTATGTCAGACCAACAGTGGGAATAATACGAGGACTGTGGATGTTGTGGTATTAG  
 AGAGTTCTGCACTGATCTGCTCCAGAGAGGGTGGTGAACAACAAAGGTACTTTCAGATGG  
 CCCAGAACATTGGCAGGCATTACTGCATATCTGCAGTGTACGCGAACACCCATGCGCAGTGG  
 GATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGGCT  
 TTTGGCGAGATGATGATTATTTCTCGCTGTCAATGTCATGTCATAGAGTTCTTTAT  
 ATGTTTAATCAGATGCCCTCAATCTTACCAATGCCGTGGCAACAGCTGCAGAGTTACTGGC  
 TTACACTGTGGAAGCAGGCACTTTTCTGACAAATGGATGTTATTTGTGGCAGAAATGA  
 TTGAAAAATTTGGAAGATTTACCAAGGAGGAAAAATCAAAGAGATTGGTGACGTGATGGTT  
 GACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCTGTGGCTGGCGCAGAGGGAAGC  
 TAAAGCCTGCAGTAGGATTGTGCAGTGTCTTCAGCGCATTGCTACCTACCGGCTAGCCGGTG  
 GAGCTCACGTTTTATTCAACATATTACCCCAATATTGCTCTGGAAGCTTATGTCACTAAGTCT  
 ACTGGCTTCAGGGGATGACCTGTACCGTGTTCAGAAAGTGGCAGCCTCTGATCGTACAGG  
 ACTTTCGGATTATGGGAGGCGGGATCCAGAGGGAAACCTGGATAGCAGCTGAGCTTTAAGT  
 GCAATGTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTATTGTACATTCTGCAATCATTT  
 AAGACTATTACAGT**TAA**ATTAGAATGATTCCTCCAAATGTTCTGCTTCGCAAAAATAACCTTATTA  
 AAAGATTTTTTTTTCGAGGAAGATAGGTATTATTGCTTTTGTCTACTGTTTTAAAGAAAAC**TA**  
 ACCAGGAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTGGCCTTTGATTCCCTTT  
 CTTACATAAAAATATCAGAAATACATTTTATAACTGCAGTGATGTAATGCAAAATATACT  
 ATTGTTACATGTGAAAAAATTTATTGACTTAAAGTTTATTATTGTTTGTCTTTTGTCTCT  
 GATTTTAAAGACAATAAGATGTTTTTCATGGGCCCTTAAAGATCATGAGCTTTTGGCACTGC  
 GCCTGCCAAGCCTAGTGGAGAAGTCAACCTGAGACCAGGTGTTTAAATCAAGCAAGCTGTAT  
 ATCAAAATTTTGGCAGAAAACACAAATATGTCATATATCTTTTTTAAAAAAAGTATTCCA  
 TTGAAGCAAGCAAAAATGAAAGCATTTTTTACTGATTTTTAAATTTGGTCTTTAGATATATT  
 GACTACACTGTATTGAAGCAATAGGAGAGGCACAACCTCCAGACCCCTAATGAACACCAATT  
 TTTTCTACTTAGCTTCTGTGGGCATGTGTAATTGTATTCTGCGGCTTTTAACTCACAG  
 TACTTTATTCTGTCTTGTCCCTCAATAATATCACAACAATAATCCAGTCAATTTATAGGC  
 TGCATAATAACTGATCCACAGGTGTTAGGTGTTCTGGTTTAGTGTGAGCACTCAATAATA  
 TTGAATGAATGACGAAAAAAGAAAAA

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**FIGURE 16**

MEPPGRRRGRAQPPLLLPLSLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK  
 VVCSSLELAQVLPDPTLPNRTVTLLSNNKISELKNGSFSGLSLERLDLRNNLISSIDPGA  
 FWGLSSSLKRLDLTNNRIGCLNADIFRGLTNLVRNLNSGNLFSSLSQGTFDYLASLRSEFQT  
 EYLLCDCNILLWMHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDPPELPSFYMT  
 SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIHNCSLIASALT  
 ISNIQAGSTGNWGCYVQTKRGNNTITVDIVVLESSAQYCPPEVVNNKGDFRWPTLAGITA  
 YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNL  
 TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVDIASNIMLA  
 DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT  
 VFQKVAASDRTGLSDYGRDPEGNLQKLSFKCNVSNFTSSSLALKVCYILQSFKTIYS

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 13-40 (type II)

**N-glycosylation site.**

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,  
 433-437, 453-457, 592-596

**N-myristoylation site.**

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,  
 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,  
 384-390, 403-409, 554-560



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**FIGURE 17**

GCGTGGGGGATGTCTAGGAGCTCGAAGGTGGTGCTGGGCCCTCTCGGTGCTGCTGACGGCGGCC  
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT  
CAGAGACATTGAGAGGCAAATTCGGAAGAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA  
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAAA  
TCATTGACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGAT  
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTGGTCACTGTCCTTTAAACTTGATCA  
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA  
GTGTGGGCAGACACTTTTGGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG  
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA  
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA  
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

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## **FIGURE 18**

MSRSSKVVGLSVLLTAATVAGVHVKKQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT  
EQLEAEREKMLLAKGSQKS

**Signal peptide:**

amino acids 1-21

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## FIGURE 19

CTGTCGTCTTTGCTTCAGCCGAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTCC  
 CAAGTGTGGCTTAATCCGCTCCACCACCAGATCTTTCCTCGGATTCTCTGCTAAGACC  
 GCTGCCATGCCAGTGACGGTAACCCGACACCACATCACAACCACCACGACGTCATCTTCGGG  
 CCTGGGGTCCCCCATGATCGTGGGGTCCCCCTCGGGCCCTGACACAGCCCCCTGGGTCTCCTTCGC  
 CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGAC  
 GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGTCTGCTTCTCCGTGACCCTGATCA  
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGCGCGAACTTCCCC  
 ATCACCTTCGCCTGCTATGCGGCCCTCTTCTGCCTCTCGGCCCTCCATCATCTACCCACCAC  
 CTATGTCAGATTCTGTGCCACGGCCGTTTCGCGGGACACGCCATCGCCGCCACCTTCTTCT  
 CCTGCATCGCGTGTGTGGCTTACGCCACCAGAGTGGCCTGGACCCGGGCCCCGGCCGGCGAG  
 ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCGTTGCCGT  
 CATCATCTTCGCGTTATCAGCGACCCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT  
 GCGTGGCGGTGTACGCCATCTGCTTTCATCCTAGCGCCATCGCCATCCTGCTGAACCTGGGG  
 GAGTGCACCAACGTGTACCCATCCCCCTTCCCCAGCTTCTGTGCGGGCTGCGCTTGCTGTC  
 TGTCTCTCTATGCCACCGCCCTTGTTCTCTGGCCCCCTTACCAGTTCGATGAGAAGTATG  
 GCGGCCAGCCTCGCGCTCGAGAGATGTAAGCTGCAGCCGACGCCATGCCTACTACGTGTGT  
 GCCTGGGACCGCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC  
 TGACCTGGTGCACCTCTGCCACCTGGTTTTTGTCAAGGTCTTAAGACTCTCCCAAGAGGCTCC  
 CGTTCCTCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTTCC  
 TCCGCCCTTCTCTGTTTTCTCTTCTGTCTCCCTCCCTCCACCTTTTTCTTTCTCTCC  
 CAATTCCTTGCACTCTAACCAGTTCTTGGATGCATCTTCTTCTTCCCTTTCTCTTGCTGT  
 TTCCTTCTGTGTTGTTTGTGTCACCATCTGTTTTTACCCCTGAGCTGTTTCTCTTTTT  
 CTTTTCTTTCTTTTTTTTTTTTTTTTTTAAAGACGGATTCTCACTCTGTGGCCAGGCTGGAG  
 TGCAGTGGTGCGATCTCAGCTCACTGCAACCCCCGCTCCTGGGTTCAAGCGATTCTCCTCC  
 CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTTCTCTTT  
 TTCCACTCTTCTTTTTTCTCATCTCTTTTCTGGGTTGCCTGTGCGCTTCTTATCTGCCTGT  
 TTTGCAAGCACCTTCTCCTGTGTCTTGGGAGCCCTGAGACTTCTTCTCTCCTTGCCCTCA  
 CCCACCTCCAAAGGTGCTGAGCTCACATCCACCCCTTGACGCGTCCATGCCACAGCCCC  
 CCAAGGGGCCCCATTGCCAAAGCATGCCGCCCACCCTCGCTGTGCCTTAGTCAGTGTGTAC  
 GTGTGTGTGTGTGTGTGTTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTTCT  
 CCCAGTGAGGAAGGTGTGAGTGTACTTCCCCCTTTAAATTAATAAATATATATATATAT  
 ATTTGGAGGTGAGTAATTTCCAATGGGCGGGAGGCATTAAGCACCGACCTGGGTCCCTAGG  
 CCCCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTGGCAGGCTTACAGAACAC  
 CCACTGCCTAGAGGCCATCTTAAGGAAGCAGGGGCTGGATGCCTTTCATCCCAACTATTCT  
 CTGTGGTATGAAAAAG

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## **FIGURE 20**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLLIILIVELCGLQARFPLSWRNFPIITFACYAALFCLSASIIYPTTY
VQFLSHGRSRDHAIATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQPALWCVAVYAICFILAAIAILLNLGECTNVLPPIPFPSFLSGLALLSV
LLYATALVLWPLYQFDEKYGQPRRSRDVSCSRSHAYVVCWDRRLAVAILTAINLLAYVAD
LVHSAHLVFVKV
```

### **Important features:**

#### **Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,  
205-226, 235-255 and 294-312

#### **N-glycosylation site.**

amino acids 66-69

#### **Glycosaminoglycan attachment site.**

amino acids 18-21

AAGCTGCGCCACGATGCCGCTGCTAATTTTGTATTTTGTAGTAGACGAGCGGTTTCACCATGTTCTCCGGCTGGTCT  
 TTGAACCTGGACCTCATCATCCGCTCACTCGGCTCCCAAAGTCTGGGATACAGCATGAGCCACATGACGC  
 CTGGCCAGCCTATGCATTTTAAAGAAATTATTCTGTATTAGTGTCGTCTAATACATTGGGCACACACAGTGA  
 AACACAGCTGAATTTCCCAAGAGCAAAACACAGTGAAGGAGAGCAACAGAAAGAAAGCAATGCAAAAGAGACA  
 TTATTACTCATCTGACTGATAGGGTCACAAATGGGGTAGCTTGATGGAGAGTGATTTTGAAGAGACACAGGAG  
 AGGACAGCATACCAAGAGAGGGGGCCAGGAAGCTCTCTGACAGAGTGGTATTTCACGCCAAACGGGAAGATGA  
 GAAAGAGCTACCGGACCATCAAAATAGTCCGAAAGAGATGGGAGAGCACTACATGACTACACTTTGGGCTGAGA  
 AATAGCATGGGATTTGGAGGAGCTGGGGGGAACCACTTTCTGCCACCTGGGGAGGAGCAATTGAGGCTTGAGA  
 AAGGGCAATGGGCAGTAGCATGAGAAGGACAGGTTAGGAGACAGGAGCTTGACAGTGGGAATCATAGTCTTAT  
 ACAGATNTGGGCAAGCAAAAGCCAGGGAGAATTTAGGTGAATGCTACGTTTGAGCCAGGCTAGATTGGGAG  
 TGGTGGGTTGATGCAAAAGGAAGAGCTCAGAAAGCAGGGCCAGACCTGGGGACAGGTTGGGGGTTTGGTTTCC  
 TTTCTCCGAGTCTCGGGAATTTGGATTGGGAAGCAAGAGGAGAGCAAGGGCCAGGGAGGAAGGAATCTTAA  
 AGAAGTCTCGATGGACCAACT  
 TTCTCGCCCTCTCTCATCTCTCTCTGGGTCTGGGAAGTGGAGCATAGCTGAAGTTTGGCTTCTGGGGGCTCT  
 TTGGAATCTCATTGCTTTCTGGGAGAGCAATTAATCACTCTCTAGCTTCTTATCATCTTACATTTCCCTGTAG  
 CCATGGGACATATGTGGTTCTGCTTCTAGCTTCCT  
 GCGGAAGTCTAAGTCTCAGAGGGGCAAGCTACTTTCTAATGTTGTACCCAAAGTGAATTTGGAGACAGAGCT  
 GCGATGCTGCCCGCTGCGGCGAGGCGCTAACTTCCAGGAGATCGCTGGCTGGCCAGGCTCTCTCGTACGTGG  
 ATGCAAGCCCTCCCATGTTCTTCTGGCCACTTTGTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT  
 GTGAGTACATGCTGGGTTCTCCCTTTCTCTCTCTGTCAGTAGAATCTACGGCCCTCTCCCAAGGCTTTCTCT  
 ACATGGATCTTAATCTACGACCTCTCCACTCTGCACTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT  
 TCCACCTCTCCCTATTCTCAGATTTTCCCAAGTGGTGAAGGACAGGCTGACCAAGCTACCGCATGGCCAGG  
 GCGGATGGCTCTGCACTATTGAGTGGGAGGGCTGACGAGCGGCACTGACCTACCTCTCTCTCTCTCTCTCTCT  
 TTTCTCTCTTATTACAGCTCAGCAGAGGGCGCAAGAGGCTCGCTTGACAGAGAGTGCTGGAGCAATTTGG  
 TCGCGGAAGCAAGCTCCGAGCATGGTCTTCGTGGATGGCGAGGACTCCATGATCATCTTATGATGAGGACAT  
 TCTGGGGGAATGGACACAGACATGCTGCGGAGCTGCCCTGGGGCCGCACTCCAGGACCTTTACCGGCC  
 ACCGCTTTCTCCGGCGCTGTGGCCAGGCTCGTGCGAGGCTGAGAGCGACTGCTCACAGACGGCTTCCCAAGACA  
 CCTGTGCTCTAGTCTGCGAGCTGGAGATGGTTGTGGGCTCCCGGCGCGCTGGGCTCCAGCTCTGCTGCTGG  
 GCGATGAGCTCTCTCTGCCAACTCGCCCCAGCCGAGGGAAGTGCTTTCCGACAGCTGGGCCACTGGAGGCC  
 AGGACTCACTCTACAATCGCCCTCAGACAGTCTGCTTTTCCCGCGGAGGAGGAGCAGCGCCCTCGAAG  
 CTCTGCGAGCAGCTCTGCCCAACCTAATGGGCACTGGGAAGCGGACCGCCAGCTCTGACCTGGCCCTCTCTG  
 GGGTGGTGTCTCTAAGTAGGAGTAGGACAGAGCAGAGAGAGCAAGACAGACACATCTGCTCGAGTGGCATCTG  
 TACCGCGCTCTGCTGACGGGGCAGAGCTCTGTGCCAAGTGTGGGCTCAAGCTCCGACAGACAGCTCCACAGC  
 TAGAGGAGCTCTGGGAGCGCTCGCTTCTCGTGTGTTTTCATGAAAGTGTGGGAGGAGGCAAGGGCTGG  
 GCTTGGGGCGACATGCTCTGCCCACTCCCGGGGCTTGGCGGGGCTGGCCGGGGCTCTGGGAGTGGCTACG  
 CAGTTGGGAGAGCATGATGTTATGTTTAAATGCCACACACATCTCTCTCGGATTAATGTGACACCTA  
 AGGGGTTGTGACTGGGCTGTGGAGGTTGGGTTGGGAGGGGCGCAGCAACCCCCACCTTCCCCATGGCTCTC  
 TTTCTCTGCTCTTTCTTTCTACTCTCCGAGTCATGTGAGTGTGATAGAATACCCCCCATGGAGGGGCTGG  
 CTCTCTGCCCTCCGGAGCTATGGGTTGAGCTGCTCTCAAGGGCCCTGCCACCTGGGCTGTGCTGTGCTCTG  
 ATTCAGCTCTCATCTGCTCTTAATTTCTCTCTTTTCTCTTAAAGACAGAAGGTTTGGTGCTGTTTCTTCTAGT  
 GGATCTTTCTCTTCTCTGGAGGCTTTGGAATGATGAAGACATGACCTCTCACTCTTCTCTGGCCGCTTAATGG  
 GGCTTGGGCGCTTTCCCAACCTCTCTAGATGTGCGGGAGTGGCTGGCGCTCAGACGACGGCGGCTGCC  
 ATTCACGCAAGCTCTCTGAGCGGGAGTGGGAAGAAGATGCTCTGTTGCCACAGAGCTCGGCATCTCATGTT  
 CTTCTAGAGAGGCGCAAGAGAGGCGACAGGGGTGCGCGGAATGTGACATGTGCTGCTGAGAGGACAGAA  
 GTTGCCAGTGAAGTGACAGTCTAGGAGGATGTCTCTTTCTGGGAGGAAGAAGGTAGAGCTTTCTGTCTGAAT  
 GAAAGGCGAAGGCTACAGTACAGGGCCGCGCCGACGAGGCTTTAATGCCACATGTTGAGGAGGCTCTGGCAG  
 ATCTGTGATCTCAAGAGTCACTGGAGTCTAGCTTTTATGTTTGGGAGGAAGGGTGGGTGCTTTGAATTAAGGG  
 CTGTAGGCTTTGGAGGTAGAGGCGCCAAAGTTAAGAACGAGAGCAAGCGGCAAGCATCTATATATAGT  
 GGCTCATAGGTGTTTATTTGTCTATTTAAGAAATTGTTTATTAATTAATAATAAAATCTTTGTAATCTC  
 TAAAA

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**FIGURE 22**

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSPKPVHMDPNYCHPSTSLHLCS  
LAWSFTRLHLHPPLSPGISQVVVDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESASFSSY  
SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG  
PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSSLCSLEDGLLGSPARLASQLLGDE  
LLLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER  
QRQASDLASSGVVSLDEDEAEPEEQ

**Signal peptide:**

amino acids 1-15

**Casein kinase II phosphorylation site.**amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,  
285-289, 324-328**Tyrosine kinase phosphorylation site.**

amino acids 44-52

**N-myristoylation site.**

amino acids 17-23, 26-32, 173-179

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

**FIGURE 23**

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCTT  
GGCACCCCTCCTGCTCAGTGCACATTGTCACACTTAACCCATCTGTTTTCTCTAATGCACGA  
CAGATTCCTTTTCAGACAGGACAACCTGTGATATTTTCAGTTCTCTGATTGTAATACCTCCTAAG  
CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA  
TACAATCTATTCTTGCCACATCAAGGGATTGTTATTCCTTTAAAAAAAACCAATACCAAAG  
AAGCCTACACATGTTGGCCTTAGCCAAAATTTCTGTTGATTTCACGTTGTTTTATTCACTTCT  
ATCGGGGAGCCATGGAAAAAGAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTT  
TTAAACCAATGGAAAAATAACCTATTCTTTTGGAAAGTGAGCAAACTTAAACTCAGATAAA  
GAAATATAAACACCTCAAATCTCAAGCGGAGTCATTCCTCTCTTGAATCTACCCAACAA  
CAGCCACGGAATAACAGATTTCTCCAGTAACCTCATCAGCAGAGCATTCTTTGGGCAGTCTAA  
AACCACATCTACCATTTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCT  
TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC  
TGCTCTGTCTTCAGAAACTTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCCTGATA  
ACAGTTCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTG  
ATAGTGGAACCAAGTGGATGGCTTACCACAACACAGTGATAGCTTCACTGGGTTTACCCCTTA  
TCAAGAAAAACAACCTCTACAGCCTACCTTAAAATTCACCAATAATTCAAAACCTCTTTCCAA  
ATAGCTCAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTTAGGT  
GCTATTCTGGGTGTCTCATTGCTTACTCTTTGTGGGCTACTTGTGTGTGGAAAAAGGAAAAC  
GGATTCATTTCCCATCGGCGACTTTATGACGACAGAAATGAACCAGTTCTGCGATTAGACA  
ATGCACCGGAACCTTATGATGTGAGTTTGGGAAATCTAGCTACTACAATCCAATCTTGAAT  
GATTCAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCTATGGATGACATACC  
TCCACTTCGTACTTCTGTATAGAACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCTACTA  
CATCCTAGCCTTTTGCAAAATTCATCTTTCAAAAGGTTACACAAAATTAAGTGTACGTTGGAT  
TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT  
CCAAAGGTTTCTTTCTTACATTTTGGCCATCCTGAGGCATTACTAAGTAGCCTTAAT  
TGTATTTTAGTAGTATTTTCTTAGTAGAAAATATTTGTGGAATCAGATAAACTAAAAGATT  
TCACCATTACAGCCCTGCCTCATAACTAAATAATAAAAATTTATTCACCAAAAAATTTCTAAA  
ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAGATTGCAT  
TTTCTTAAATGAAAATTGAAAGGGTGTCTTTTAAAGAAAATTTGACTTAAAGCTAAAAGAG  
GACATAGCCAGAGTTTCTGTTATTGGGAATTTAGGGCAATAGAAATGACAGACCTGTATTCT  
TAGTACGTTATAATTTTCTAGATCAGCACACATGATCAGCCCACTGAGTTATGAAGCTGA  
CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCCTACCCAGGAAAGTAATAGCT  
TCTTTAAAAGTCTTCAAAGGTTTTGGGAATTTTAACTTGCTCTTAATATATCTTAGGCTTCAA  
TTATTTGGGTGCCTTAAAAACTCAATGAGAATCATGGT

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## **FIGURE 24**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732

><subunit 1 of 1, 334 aa, 1 stop

><MW: 36294, pI: 4.98, NX(S/T): 13

MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENI  
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSEFVSKVPWNA  
PIADEDLLPISAHFNATPALSSNFVWVSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE  
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFNPTSDPQKENRNTGIVFGAILGAIL  
GVSLTLVGYLLCGKRKTDSFSHRRLYDDRNEPVLRLDNAPEPYDVSGNSSYYNPFTLNSA  
MPSEENARDGIPMDIPPLRTSV

### **Signal peptide:**

amino acids 1-23

### **Transmembrane domain:**

amino acids 235-262

### **N-glycosylation site.**

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,  
163-167, 218-222, 225-229, 298-302, 307-311



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**FIGURE 25**

AACAGGATCTCCTCTTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC  
 AGCCCGAAGATTCACT**ATG**GTGAAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG  
 AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC  
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT  
 CTTAGGCCCTTTCATTTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT  
 TCATGCCCAAGAGCACCATTTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA  
 AATTCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGA  
 GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCCCTG**C**AG  
 CAATTATTTCATGACTTTGAAAAGGGAATGACTGCCTTACCTGGACTTGTGCTGGGGAACTGC  
 TATCTGATGCCCCCTCAATACTTCTATTGTTATGCCTCCAAAAATCTGGTAGAGCTCTTTGG  
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTATGTGGTTCGAGAAGACCTAGTTGCTG  
 TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA  
 AAGTCCCTCCGCCTTCGTGCGCAGAGACCTCTGTGGGTTTCAACAAACGTGCCATTGATAA  
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAGT**T**  
**A**AGAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA  
 CATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT  
 AAAAAAGGAAAAAAAAAAAAAACTACTAACCACCTGCAAGCTCTTGTCAAATTTTAGTTTAAT  
 TGGCATTGCTTGTTTTTTGAAACTGAAATTACATGAGTTTCATTTTTTCTTTGCATTTATAG  
 GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATCCATCC  
 GTTGTTTTTTTTGTTTGTGTTTTTCTTTTCTTTAAGTAAGCTCTTTATTCATCTTATG  
 GTGGAGCAATTTTAAAAATTTGAAATATTTTAAATTGTTTTTGAACCTTTTGTGTAAAAATATA  
 TCAGATCTCAACATTGTTGGTTTCTTTTGTGTTTCATTTTGTACAACCTTCTTGAATTTAGA  
 AATTACATCTTTGCAGTCTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT  
 TTCATGAGACAGTCATTTTTAACTAATGCAGTGATTCCTTCTCACTACTATCTGTATTGTGG  
 AATGCACAAAATTTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATCTACAA  
 CCCTATAATAAATTTTACTCTATACAAAAA

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**FIGURE 26**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVEALLSRTVRTQILTGKELRVATQEKEGSSGRCLMTLLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDSDPAAIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPKKNLVELFGKLAGS
RYLPQTYVVREDLVAVEEIRDVSNLGIFIYQLCNNRKSFRLLRRDLLLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE
```

**Type II transmembrane domain:**

amino acids 53-75

**N-glycosylation site.**

amino acids 166-170

**Casein kinase II phosphorylation site.**

amino acids 35-39, 132-136, 134-138

**N-myristoylation site.**

amino acids 66-72, 103-109

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 63-74

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**FIGURE 27**

GGAGGAGGGAGGGCGGGCAGGCCAGCCCCAGAGCAGCCCCGGGCACACGACGACTCTCT  
 CTTCCAGCCAGGTGCCCCCCACTCTCGCTCCATTGCGCGGGAGCACCCAGTCTGTACGCC  
 AAGGAACGGTCTGGGGGCACCATGTTTCGGCGGCAGCCCCAGCCTCTCATCTTCTG  
 TTGCTGCTGCTGGGGTCTGTGCCTGTACCGACGCCCCGCTCTGTGCCCCGTAAGGCCACGTT  
 CCTGGAGGATGTGGCGGTAGTGGGGAGGCCGAGGGCTCGTCGGCCTCTCCCCGAGCCTCC  
 CGCCACCCTGGACCCCGCCCCCAGCCCCACATCGATGGGGCCCCAGCCACAACCTGGGG  
 GGCCCATCACCCCCACCAACTTCCTGGATGGGATAGTGGACTTCTTCGCCAGTACGTGAT  
 GCTGATTGCTGTGGTGGGCTCCCTGGCCTTCTGTGTATGTTTCATCGTCTGTGCCGCGGTCA  
 TCACCCGGCAGAAAGCAGAAGGCCTCGGCCTATTACCCATCGTCTCTCCCAAGAAGAAGTAC  
 GTGGACCAGAGTGACCGGGCGGGGGCCCCCGGCCTTCAGTGAGGTCCCCGACAGAGCCCC  
 CGACAGCAGGCCCGAGGAAGCCCTGGATTCTCTCCGGCAGCTCCAGGCCGACATCTTGGCCG  
 CCACCCAGAACCCTCAAGTCCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG  
 GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGCAGCCAGGAGGGGGACAGGAAGTCCA  
 GGGACATGGGGTCCAGTGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCTTGG  
 AGGGGGCTGTGGTGGCCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTAGCCAG  
 GAAGCCCAGGGACCAGTGGGTCCCCCGAAAGCCCTGTGCTTGCAGCAGTGTCCACCCAG  
 TGTCTAACAGTCTCTCCGGGCTGCCAGCCCTGACTGTGCGGCCCCCAAGTGGTCACTCCCC  
 GTGTATGAAAGGCCTTCAGCCCTGACTGCTTCCTGACACTCCCTCCTTGCCCTCCCTGTGG  
 TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGCTGCCCGGA  
 GGAATCTTACCAAGTGCCATCATCTTACCTCAGCAGCCCCAAAGGGCTACATCTTACAGC  
 ACAGCTCCCCTGACAAAGTGAGGGAGGGCAGCTGTCCCTGTGACAGCCAGGATAAAACATCC  
 CCCAAAGTGTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCAAACTACTTTTTAAACA  
 GCTACAGGGTAAAACTCTGCAGCACCCACTCTGGAAAATACTGCTCTTAATTTTCTGAAGG  
 TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTTAAATCCTC  
 TCAAGCGCTCTCCAAGCACCCCGCCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGCTGG  
 GATCAGGTTGAATGAATGGAACCTCTCCTGTCTGGCCTCCAAGCAGCCTAGAAGCTGAGGG  
 GCTGTGTTTGAGGGGACCTCCACCCTGGGGAAGTCCGAGGGGCTGGGAAGGGTTTCTGACG  
 CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCTGTGCTCACACATTGTCTGGCAGCCTG  
 TGTCACAATATTCTGTCAGTCTCTGACAGGGAGCCTGGGCTCCGTCTGCTTTAGGGAGGCT  
 CTGGCAGGAGGTCTCTCCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT  
 CCAGGTGCTGAGATATAATGCACCAGCACATAAACCTTTATTCCGGCCTGAAAAAAAAA  
 AAAGA

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## **FIGURE 28**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop .
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAPSLILLILLLLGSPATDARSVPLKATFLEDVAGSGEAE GSSASSPSLPPPWTPAL
SPTSMGPQPPTLGGPSPPTNFLDGIVDFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLAQEAQGPVGPESPACSSVHPSV
```

### **Signal peptide:**

amino acids 1-25

### **Transmembrane domain:**

amino acids 94-118

### **N-myristoylation site.**

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,  
211-217, 238-244, 242-248

[illegible]

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## **FIGURE 30**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGFLACLLALCLGSGEAGFLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDEVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGLGGQGNPGLGTPWVHGYPGNSAGSFGM
NPQGAIPWGGGNGGPPNFGTNTQGAVAPPGYGSVVRASNQNEGCTNPPPSGSGGGSSNSGGGS
GSQSGSSSGSGSNGDNNNGSSSSGSSSSGSSSSGSSSGSSSGSSSGNSGGSRGDSGSESSW
GSSTGSSSGNHGSGGGNGHKPGCEKPGNEARGSGESGIQGRFGQGVSSNMREISKEGNRLL
GGSGDNYRGQSSWGSGGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDINKDQ
RSSRIP
```

### **Signal peptide:**

amino acids 1-21

### **N-glycosylation site.**

amino acids 265-269

### **Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

### **Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

### **N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,  
74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,  
155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,  
218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,  
249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,  
279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,  
295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,  
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,  
383-389, 387-393, 389-395, 395-401

### **Cell attachment sequence.**

amino acids 301-304

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**FIGURE 31**

GACCGGTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCCGCGGGCGGTGCTCACC  
 TGCCCTGGCTGGTGGAGTTTCTCTCCTTGTCTGACCATGTTGTTCCCTTGTCTGGAATATTACCGGGACATCTTCA  
 CTCTCCTGCTCGGCGCTGCACCGGAGCTTGGTGTGTGCGAGGAGAGTGAAGGGAATGTTGTTTCTTGAACAAGC  
 TGCTGCTACTTGTCTGCTCTGGGCTGGCTTTTCCAGATTCCCACAGTCCCTGGAGCACTGTTCTTCTTGGAGAGG  
 GTCCCTCATATGCGCTTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTTGGACAATGCGCCTGTGTGGACACG  
 AGCTGCTCTACACCTGCTGCCCTACATCGGAGAGCTCCGGAACCTGCTCGCTTCTGTTGGGTGTCAAGCAGTAGTG  
 GACGGAGTGGGGCTTCTAGGGAATAACACCCACCCTACACAGCTGGGAGCCAGCCTTCCAGACCA  
 GCCAGGGGCTCGAGGCACAGCTCGGCCAGGCCTTTTCCACAACACAGCGCCCTCTTGGCGCGGACCGCTAGAGT  
 TCGTGGCAGAAAGAAATGGATCAAACTGTGTCAACATATCAAGGCTACACTGGTGGCAGATCTGTTGGCGCCAGG  
 CAGAGTCACTTCTCCAAGACAGCTGGTGACACAGGAGAGGAAGGGGGAGACCCAGCCAGCTGTTGGAGATCT  
 TGTGTTCCACAGCTGTGCCCTCACGGGGCCAGGCATTGGCCCTGGGCGGGAGTTCTGTCAAAGGAAGAGCCCTG  
 GGGCTGTGCGGGCGCTGCTTCAGAGGAGACCCCGGACGCCCTTCTGAGCAGTGCAGAGAATGCTGTGGGGC  
 TTGCAACAGAGAAAGCCTGTGCTTGGCTGTACGCCAACATCACAGCACTGATCAGGAGGAGGTGAAGACAGCAG  
 TGAGTCGCACACTTCGAGCCACAGGTCCTGAACCTGCTGCCCGGGGGAGCGGAGGGGCTGCTCCCGCGCTGAC  
 GTGCTCTCCTTGGCCGTGGGGCCACGGGACCTGACGAGGGAGTCTCCCAGAGCATCTGGAACAGCTCCTAGGC  
 CAGCTGGGCCAGAGCGTGGCGTGGCGCCAGTTCCTGTGCCACCTGCTGAGCAGCATCTGGCAAAGTCTCTGTG  
 GAGTTAGCTTCCCTCCTCGTTGCAGATCAAAATTCCTATCCTAGGCGCCCGGCACAGTACAGGCTGGAGAGAGG  
 CAGGCTCGAAGGCTTCTGCACATGCTCTTCTTCTTGGAGGAAGACTTTCAGGGGCGGTTCCGCTGCGAGCTG  
 CTGCTGAGCCCAAGAAATGTGGGCTTCTGGCAGACACAAGGCCAAGGGAGTGGGACTTGGCTGTATTCTTGTCTA  
 CGGGAGCTGTTGGAGAAGGTTCTGATGGGACGGATGGAGATAGAGGCTGCTGGCGAGCCTCCACAGGCCGAC  
 TGGCCAGGGGACTTGTCTGAAGAATTAGCAACACTGTCTAATCTGTTTCTAGCCGAGGCCCACTCGCAAGACCC  
 CAGCTAAGAGCCTGTGAGTTGGTGCAGCCAACCGGGGCACTGTGCTGGCCAGAGCTAGGGCTGAGAAGTGCC  
 CTGCTTGGCGATTGCACAGAACCTGAGCCCCGCTCACGAGGAGGCCAAGTGCCCAATGCACAGCCCTCAC  
 TGGTTGGGGTGTAGCTGGGTCTACAGTCAGACTTCTGCTCTAAGGGTGTCACTGCCCTGGCATCCCAACGCGA  
 ATCCTTAGAGGAAGGAGAGTGGCTGATTGGGATTATGGCAGAAAACTCAGAGAGCGAGCTCGGAGTAGAA  
 GAGGTGGTGTGTTTATCTCTTGGATACTAAATGAATGAGGTGTGTGGGCTTGTCAACACAGAATTCAGCCT  
 CATTTGCTATCCAGCATCTCTTAAACTTTGTAGTCTTGAATTATCATGACAGGCAAAATGACTCTCGCTTAAC  
 TTATGAAGAAAGTTAAACATGAATCTTGGAGTCTACATTTCTTATCACCAGGAGCTGGACTGCCATCTCCTT  
 ATAAATGGCTATAACACAGGCGGGTCTGTTGGTGTGCTGTAAATCCAGCTACTCAGGAGGATGAGGACGAGACTGCTGAAC  
 TATTAGCTGGGCATGGTGGTGTGCTGTAAATCCAGCTACTCAGGAGGATGAGGACGAGAGACTGCTGAAC  
 CTGGAGTGAAGGTGTCAGTGAAGCCGAGGTGCGACCACTGCACTCCAGTCTGGGTACAAGAGGAGACTTCTGAG  
 AAAAGCCTAACAAACAGATAGGTAGGACTCAACCACTGAACCTGACTTTCCTCTGTACCTCAGCCCTG  
 TGCAGGTAGTAACCTCTGAGACCTCTCCCTGACCAGGGACCAAGCAGAGGCACTTATAGAGCTTTTATAGATAAA  
 TGGGTTTTTTTAAAAAAGGGCTTTATTAATAATCTCCCCACACGATGGCTCCTGCAATCTGCCACAGCTC  
 TGGGCGGTGCTGTAGGGAAGAGCCCTGTTTCCCTGAGCGGGGCTGGGCTGTGCATGGGTGCGGGAGCTG  
 GCCGTGCTTGGCCCTTGGCGTGTGTCTAGCTGCTTGTGCCGGGCACAGAGCTGCGGGGTGTGGGGCAACCGG  
 AGCTAAGAGCAGGCTCTGGTGCAGGGGTGGAGGCTGTCTTAAACGACACCCCTGAGGTGCTCTGTAGATGCTG  
 GTTCCACCTGAGTGGCAGGGGAGCAGCTGTGGCCGTGCTCTCTCYTAGGCACAGTCTTGGGGAACTAAGCTC  
 GGGCCCTTCTTGAAGACCGAGAGTGGGTGGGTGTGGGGAGTGGCCTGAGGAGCTACGTG  
 GAAGAGGCGCGGGTTGTGGCTGCAGCGGCTGGAGCGCTCTCTCTGAGCCTCAGTTTCCCTTCCGCTCA  
 ATGAAGACATGCCCTCTCGTGTCTCAGGCTATTAGGACTTGCCTCAGGAATGGCCTTGGACGAGCTCAT  
 GTTATTTTCACACTGCTCTGCGACGTTGGCTGGGCACGTGATGGAATGGCCATGTCCCTCTGCTGCGTGGAC  
 GTTCCGCTGGGAGTGCGCAGCCAGAGCGGGCCAGACGTGCGCTGGGGTAGGGGAGGCGCCGAGGAGG  
 CCTCACAGGAAGTTGGGCTCCCGCACCAACAGGCAGGCGGGCTCCCGCGCCGCGCCGCCACCACTGACG  
 GCGCGGTAGACAAAGTGAAGTTCGCGCTTGGGCTGCTGCGCAGAGTGAAGCTTGTATGACAGTGGCGAGCGG  
 TCGTCCGCGAGCTGGAAGCAGCGCCGCTCCACCAGCAGAACAGCCGCTGCGCCT

## **FIGURE 32**

MCFLNKL LLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC  
CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP  
SLRRTVEFVAERIGSNVCVKHIKATLVADLVRQAESLLQEQLVTQGEEGDPAQLLEILCSQL  
CPHGAQALALGREFCQRKSPGAVRALLPEETFAAVLSSAENI AVGLATEKACAWLSANITAL  
IRREVKA AVSRTLRAQGFEP AARGERRGCSRA

### **Signal peptide:**

amino acids 1-18

### **N-glycosylation site.**

amino acids 244-248

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 89-93

### **Casein kinase II phosphorylation site.**

amino acids 21-25, 167-171, 223-227

### **N-myristoylation site.**

amino acids 100-106, 172-178, 207-213

### **Microbodies C-terminal targeting signal.**

amino acids 278-282



## FIGURE 33

TCCCTTGACAGGCTCTGGTGGCTGGTTGCGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG  
AAGACTCTCTGCTTTTGGCCACAGCAGTTCCTGCAGCTTCCTTGAGGTGTGAACCCACATCCC  
TGCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAAATG  
AGTAGCAACAAGAGCAGCGGTGACAGTGTTCGTGATCCTCTTTGCCCTCATCACCATCCT  
CATCCTCTACAGTCCAACAGTGCCAAATGAGGTCTTCCATTACGGCTCCTCGGGGGCCGTA  
GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCTTCTCGGC  
ACAAGACACTGCCCTCTCGGTGCCACCAAGTGTGTGATTGTCAGCAGCTCCAGCCACCTGCT  
GGGCACCAAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC  
CCACCCTGGCTACTCAGCTGATGTGGGCAACAAGACCACCTACCGCCTCGTGGCCCATTC  
AGTGTGTTCCGCGTGTCTGAGGAGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGT  
CATCTTCTGGGGGCCCGGAGCAAGATGCAGAAGCCCCAGGGCAGCCTGTGCGTGTGATCC  
AGCGAGCGGGCCTGGTGTTCGCCAACATGGAAGCATATGCCGTCTCTCCCGCCGATGCCG  
CAATTGACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCGTGGTT  
GAGCACAGGCTGGTTTACCATGTGATCGCGGTGGAGTTGTGTGACACAGTGCATGTCTATG  
GCATGGTCCCCCAACTACTGCAGCCAGCGGCCCGCCTCAGCGCATGCCCTACCACTAC  
TACGAGCCCAAGGGGCCGACGAATGTGTACCTTACATCCAGATGAGCACAGTCCGAAGGG  
CAACCACCAACCGCTTCATACCCGAGAAAAGGGTCTTCTCATCGTGGGCCAGCTGTATGGCA  
TCACCTTCTCCCAACCCCTCCTGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG  
AGGAGAAGCAGCCTCCGCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTG  
CTGGAGTGTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC  
TGGGGAATCTTGTGGCAATCAGGGATTGGGAGTCTATGTGGTTAATCAGGGGTGCTTTTC  
TTGTGACAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGGTATTCTGAGTCAATCTG  
AGGCTAAGGACATGTCTTTCCCATGAGGCCTTGGTTGAGAGCCCCAGGAATGGACCCCCCA  
ATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCCAAGGAGCTGGGAATCTGGTGTG  
CCCCCTCAATTTCCAGCACCAGAAAAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCC  
GGCCAGAGAATTGTGGGGTTGTGGAGTTGTGGGGGGCGTGGGAGGTCCAGAGGTGGGA  
GGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTGGAACAAACCTTCCCCCTCTCTGGG  
CACCTTCTGCCACACCAAGTTTCCAGTGGGAGTCTGAGACCCCTTTCCACCTCCCCACAA  
GTGCCCTCGGGTCTGTCTCCCGTCTGGACCTCCAGCCACTATCCCTTGTGGGAAGGT  
CAGCTCTTTGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAACCTTAGGGTATTTTTCG  
GCAACTCCTTCAGGTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCT  
TAGCCCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCCTCCTTTCTGCCCT  
CTAGCAGGGAGGTTTTTCCAATGTTGGAGGCGCCTTTGGGGCTGCCCCCTTTGTCTGGAGTCA  
CTGGGGGCTTCGAGGGTCTCCCTCGACCTCTGTCTGCTCGGATGGCTGTGCGGAGCTGT  
ATCACCTGGGTCTGTCCCTGGCTCTGTATCAGGCACCTTTATTAAGCTGGGCCCTCAGTGG  
GGTGTGTTGTCTCTGTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA  
GGCTGGAGGGACCATGAGATGGAGAGGCCAGCAGCTAGCCATTGCACACTGGGCTGATGGGTGG  
GGGCGGTGACTGCCCCAGACTTGGTTTTGTAATGATTGTACAGGAATAAACACACCTACGC  
TCCGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 34**

MSSNKEQRSVAVFVILFALITILILYSSNSANEVVFHYGSLRGRSRRPVNLKKWSITDGYVPIL  
GNKTLPSRCHQCIVIVSSSSHLGLGPEIERAECTIRMNDAPTGYSDVGNKTTYRVVAH  
SSVFRVLRRPQEFVNRTFETVFIWGPSPKMQKPQGSLVRVIQRAGLVFPNMEAYAVSPGRM  
RQFDDLFRGETGKDREKSHSWLSTGWFTMVI AVELCDHVHVYGMVFPNYCSQRRLQRMPYH  
YYEPKGPDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 9-31 (type II)

**N-glycosylation site.**

amino acids 64-68, 115-119

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 50-54

**Casein kinase II phosphorylation site.**

amino acids 3-7, 29-33, 53-57, 197-201

**Tyrosine kinase phosphorylation site.**

amino acids 253-262

**N-myristoylation site.**

amino acids 37-43, 114-120, 290-294

**FIGURE 35**

GTTTTCATAGTTGGCGTCTTCAAAGGAAAAACACTAAATGAGGAATCAGCGGACCGGAGGACGACAGCTT  
 GAGGACATGCTACCTAGCTGTTGGCCGACGAGGGGAGAGCTGAAGCCAGCTGGCCGAGTCTCTCAGGGGCTGG  
 GCGAAGGTGAAAGAGCTTTCAGAAACAGGCTTCTGGAACCATGACCCATGAAGTCTTGTGCATATTTATACCCT  
 CTAGGGTAGGACAGCTGAAACTAGAGAAATGGAGTGTGGCGAGGACGGCAGTATCTTTTGTGTGACCTTGGC  
 GGCCATGGAGCTTGGCTCAGACCTTTGTGTACACCATCTGGTGGGAGAGCATGACGGCGTGGAGAGGAATG  
 AGGCTGTAGGTCAACATGCTTGGCTCTCTCAGCCACGAGGAGCTGTTTGGTACTTGAACAGAGGTCTCTCAG  
 CTACCGCTCAGGCTGGCTCCACCTGCAGAAAGCCGAGGAGCATGTGATCTTGGGCTGCTGGTGGTGAACCTCCA  
 AGGATGAATGTAACTGGGCGCTGAATGGAAAGAGCTAGATGTCTCGATAGTACTCTGGGTGTCTCTCATCAC  
 CGGCTGGTGGCTGCTCATCTGCCCTTAAACAAACACATCTGTGGAGCAGGTACAGTGTGTGGCCGGGTGCTCGCG  
 GCGCTGGTGGCTGCTGCTGAGCTTCTGAGCTTCTCAATCTCAGAGCTCAAGTGTAGATGTGACAGCACT  
 ATTGAAGTGGATGGGAAACACAGCACTGCTGAGTCTGAGTCTGAGCTTCTGAGCTTCTGAGCTTCTGAGCTTCT  
 TACAGCGCTCAAAACAGAGATGGCTGGAGGCGCTCAGAGATTAACCTCTGAGTCTGAGTCTGAGCTTCTGAGCT  
 TGAATGGCGACGAGGAGGACGAGGCAATGTACAAGTGTGAGCTTCAACCCAGTACGACGAGGAGTAAAC  
 TCCGGCTCAGCGACAGGCTAGCTGGCGCGCTCACCGCTGAGGCTCCGCATCATCTACCCCCAGAGGCC  
 CAACACATCATCTGTCAAAAGGCCAGAGTCTATTCTTGAAGTGTGTGGCAGTGGAAATCCCAACCCAGGGGT  
 ACCTGGGCGAAGGATGGGTCAAGTGTCAAGCTGTCAACAAAGACGGCTTCTCTGTGAGCAACTCTCTCATCTGAC  
 ACACAGCAGGAGGAGATCAGGCACTACCGTCACTGGCCAGATGGGTGGGCGCCGGGAGCGGCTGCT  
 ATCTCTACAATGTTCAGGTTGTTGAACCCCTGAGGTACACCTAGGACTCATCCAGCTGGTCACTCCCTGGGGC  
 CAGAGTGGCCAGCTTACCTTGTAGGTGGTGGGAACCCCGCGCTCGTGGTGTGGTGGAGGAATGCTTGTGCC  
 GTCTACCACTCATGGCAGAAAGAGTGTGGAGGCGCTTCGCGTGTCTCAGTACGCTGGGCGCTGAGGACAGAGC  
 ATAAACCCAAAGCTTGGCAGATGCTGACTGCTGACTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT  
 CTTGACGAGATGCTGAGGGGGCAACCGCGCGCTCCCAAGCCCCAAGCTCAGTGGGCGCTGCTCTCGGAGT  
 CAGGAGAGAGAGGGGCAAGGGGCTCCCGCGAGGCTCCCATCATCTCAGCTTCGCGCCAGCTCCAAGACAGAC  
 TCATATTGAAGTGTGTGGCGGCTCGCATTTGAGGCACTGGCCGGGCGCAATCTCTACTATTGTGTGAACAC  
 CGAAGCAGGCTCAAAATCTCTTCGAGTATGGACATCTGCTGCTTACAGCAACAGCAGCGCTGACCTGACCT  
 ACAGACTTGAACCCGGGAGTGTGTGATGAAGAGATGGAGCTTACAATCTTGGGAGGAGGGGCAAGCGACT  
 ATGCTCACCTTCTCGAATGGAGCGGCGCAACCCGAGTATGCGCCAGCAAGAGCAGAGATCAGAGAGAG  
 CTTGAGGAGCAGCTCCGAGAGCAGGACGAGCAGACGCGGCTCTCCCCCAAGAGCTCCGACAGG  
 CCGACAGTCTGAGGAGCTTCTGAGAGCTCAGTGTGAGTGAATCTCCCGTGGGAATGTGGGTTCCCAATC  
 CAGTCTTCCCTGTGGATATGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGT  
 TCGGGCTTCCGTGGAGATCAGCGGCTTAGAAGAACTCTCTAAGTATGAGTGTGAGGAGTGTGAGGAGT  
 CTGGGGAGAGCGAGGCCAGCGCCCTCTCTCGGCGTACGTGTGTCTGCGGCTACAGCGTGCCTGTACAGAGAT  
 CCGTGGGAGTCTTATATCACTTCAGGATGGCGTCTTAATGAGACCACTCATGCTCAAGTGGATGTACATC  
 CAGCAAGTATCAACACACACCCCAATCATGCTTTATGTCTATTATTACCCACAGACAGTGAATATGATG  
 GACTACAGAAAGGATATGTTGGAAAGGGCAAGTATGGCACTCATGAGCCATCGAGCCAGTCAAGCAGCACTCTTAC  
 GACTATAGATGTCAAGTCTTCAATGAAGAGGGAGAGCGAGTTCAGCAAGCTGATGATCTGTGAGACAGGCT  
 CGGAAGTCTTCTGGGCAAGCTGTGTCAGCTGCGACCCCAACTCTGGCCCCACAGCGCCCTCTCTGAAAC  
 ATTAAGCGCGGTGGGACCTGGGCGCTGTGGTGTGCTTCAGGAGCACTGCCATCTGTGTTGTGGGTGCT  
 TGAAGTGTGGGCTGCTGCTGAGTCTTCTGAGTCTTCTGCTTCTGAGGAGGCTGGTCTTAAGCAAAAACTC  
 AACAACAGCTGGCTTCTCTGAGTGTGAGTCTTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT  
 CAGGCGACAGCGAGTGGAGACCCCTACTCATGTCGATCAGTGGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT  
 AATGAGGGGTGACCTCTGGCTGCTGAGTGGGTACCGCGGATGAGGCCACAGCACTTCCAGCGGAGCTTCAG  
 CAGAGATGTACACAGGAGCTGTGGAGGACACCATTTGGCAATGGATATGACCCCAAAGTACAGAGATC  
 ACAGGGGTCCCAAGTCTAGCCCGCAGGAGGCTCTTTCTTATACACGTCCCGAGCACTCCATCAACAGCT  
 CTGGGCCCCATCAGACTGTCTGCAACCGAGGAGACAGCTGTGCTGTGGCCGATCAGGGGTGAGGAGGCC  
 CGCAGACTCTCTGTCTGGAAGCAGTGGGACCTCATTTCACTCAGGCGCCCATGCTGCTTGGGCTTGTG  
 CCAATTGAAGAGTGGACATCTGACTCTGCAAGTGAAGTGAAGAGACTGTGTCGCCAGACCCGTGAGG  
 CTTGAGTGAAGCAGGAATCTGGAATGTGAGTCTCTCCCGGGCCACTGGTGGGTGTCTTTGAAACACCACTC  
 CTTGAGTGAAGTGAATCTGCAAGAGTATCTCAACAGAGATATATATTGTTTTTTTTTAAAAAATAAAGAGAAAA  
 AGAGACAGAAATATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAAT  
 TATGTTTATATATCTTGAGAGATCAAGAGATCTGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAAT  
 CTTAACAGAGTCAACGGAAGACCCACAGCTGCGCGGAGGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAAT  
 GAGGCGAGGTCTGAGGAGGCCACAGATAGCTGGCAAGAGGAAGTCCAGGACAGGAGTCTATCAGCAGCA  
 TAGGAAACAGCAGAGGGGCCAGTATCACAGCTGGAGACACCCACAGATGCTGGATCGGCTGCTGAGGAA  
 CAAGTTTCTTAAGTGGCATGAGAAACAGCAAGATGTGTACAGCATATGAGCATTAATAAATCTTCCCAAT  
 CAATAATTCGTGGCAACATATCTCTGAAAAAACAACACTGTAACCTTAATAATGTTAGTCTTCCGTGTAAAT

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# **FIGURE 36**

MLRGTMTAWRGMPEVTIACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVILGCVVEPP  
 RMNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL  
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPSGNLQ  
 IVNASQEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEAAARI IYPPEAQTIIVTKGQSL  
 ILECVASGIPPRVPTWAKDGSSVTGYNKTRFLLSNLLIDTSEEDSGTYRCMADNGVGQPGA  
 AVILYNVQVFEPPEVTMELSQLVI PWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS  
 RRALRVLSMGPEDEGVYQCAENEVGSAAHVQLRTSRPSITPRLWQDAELATGTPPVSPSK  
 LGNPEQMLRGQPALPRPPTSVGPASPKCPGEGKGQAPAEAPIILSSPRTSKTDSYELVWRPR  
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE  
 GQTAMVTFRTGRRPKPEIMASKEQQIQRDDPGASPOSSSQPDHGRSLSPPEAPDRPTISTASE  
 TSVYVTWI PRNGGGFIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRV  
 RALNMLGESEPSAPSRPYVVS GYSGRVYERPVAGPYITFTDAVNETTIMLKWMIIPASNNNT  
 PIHGFIYYRPTSDNDSDYKMDMVEGDKYWHSISHLQPETS YDIKMQCFNEGGESEFSNMV  
 ICETKARKSSGQPGRLPPPTLAPPQPPLPETIERPVGTGAMVARSSDLPYLI VGVVLGSIVL  
 IIVTFI PFCLWRAWKQKHTDLGFP RSALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA  
 CANGIHMNRGCP SAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLNGYDPQSHQITRGPK  
 SSPDEGSFLYTL PDDSTHQLLQPHHDCCQRQEPPAAVGS GSVRRAPDSPVLEAVWDPPFHSG  
 PPCCGLVPVEEVDSPDSCQVSGGDWCPQHPVGAYVQGEPGMQLSPGLVLRVVSFETPPLTI

## **Signal peptide:**

amino acids 1-30

## **Transmembrane domain:**

amino acids 16-30 (type II), 854-879

# FIGURE 37

CGGGAGGCTGGGTGCTGATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTC  
 CCAGGCTCCCGCGGCGGACCCCGCGCAAC**ATG**CAGCCACGGGCGCGAGGGTTCCCGCGC  
 GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC  
 CCGTAACCCGCGCGGAGACCAGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCCC  
 AGCCTCTTACCACGCCGGGTGTCCCAGCGCCCTCACTACCCAGGCCTCACTACGCCAGG  
 CACCCCCAAAACCTTGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG  
 TGGACGGCCACAATGACCTGCCCCAGGTCCTGAGACAGCGTTACAGAATGTGCTTCAGGAT  
 GTTAACCTGCGAAATTTTCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT  
 GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC  
 TCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCTCCTACTCTGAAGCTCGAGCTT  
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTGGCGTGNAGGG  
 TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGTGCGCT  
 ACCTGACACTTACCTTCACCTGCAGTACACCATGGGCAGAGAGTTCCACCAAGTTTCAGACAC  
 CACATGTACACCAACGTCAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA  
 CCGCCTGGGCATGATGATAGATTTGTCCATGTCATCGGACACCTTGATAAGAAGGGTCCTGG  
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTTG  
 TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAAGGTGGCATCGTGATGGTGACACT  
 GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG  
 ACCACATCAGGGCAGTCATTGGATCTGAGTTTATCGGGATTGGTGGAATTTATGACGGGACT  
 GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCT  
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCCTTCGTGGAACCTGCTGCGGGTCT  
 TCAGACAAGTGGAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCGTGGAGGCTGAGTTT  
 CCATATGGGCACTGAGCACATCTGCCACTCCACCTCGTGCTCAGAAATGGACACCAAGGC  
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCTGGAGGTCTCAAAATGCCT  
 CCCCATACCTTGTTCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTCAACCAAGTGGCTC  
 TGCT**GA**CACAGTCGGTCCCGCAGAGGTCACTGTGGCAAAGCCTCACAAGCCCCCTCTCCT  
 AGTTCATTACACAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA

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## **FIGURE 38**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLLLLLLLLLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWSASVSCSQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVRRESRAQSPVEAEFFYQGLSTSCH
SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPFTTQWLC
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-36

#### **Transmembrane domain:**

amino acids 313-331

#### **N-glycosylation sites.**

amino acids 119-122, 184-187, 243-246 and 333-336

#### **N-myristoylation sites.**

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 136-146

**FIGURE 39**

TGCTAGGCTCTGTCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA  
 TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCAGCAAGCCTGATAAG**ATG**  
 AAGCTCTTATCTTTGGTGGCTGTGGTCCGGTGTGCTGGTGCCCCAGCTGAAGCCAACAA  
 GAGTCTGAAGATATCCGGTGCAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA  
 TTTACAACCAGAATGTATCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA  
 GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG  
 CACCACCACCATCAAGGTCATATTGTCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT  
 ACATGGCCTTCCTGATGCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA  
 CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG  
 GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGC  
 AGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGCT**TAGAT**GGGCTGG  
 TGTGGTTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAGCAGGGGG  
 CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCCTGTGGCATTCTTCTCCTT  
 CTCCCTAACTTTAGAAATGTTGTACTTGGCTATTTGATTAGGGAAGAGGGATGTGGTCTCT  
 GATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAGGGAGGGGGAAGGCAGGCCAGAAGGGA  
 ATGGAGACATTCGAGGCGGCCCTCAGGAGTGGATGCGATCTGTCTCTCTGGCTCCACTCTTG  
 CCGCCTTCAGCTCTGAGTCTTGGGAATGTTGTTACCCTTGAAGATAAAGCTGGGTCTTCA  
 GGAACTCAGTGTCTGGGAGGAAAGCATGGCCAGCATTACAGCATGTGTTCCTTCTGCAGTG  
 GTTCTTATCACCACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG  
 AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCCTGGA  
 AGCTGGTGTTCGCTGTCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT  
 CTGCTGCCGTTCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTG  
 CACAGTCACTGAGCCAGACGGTTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA  
 CACCACAGCCCCGTACTTGGGTTCCTCTGTCCCTGAACCTTCGTTGTACCACTGATGATGA  
 GAGAAAATTTTGTCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAATTTG  
 TTTTATTTCTCTCA





**FIGURE 41**

AGCGGGTCTCGCTTGGGTTCCGCTAAATTTCTGTCTGAGGCGTGAGACTGAGTTCATAGGGTCTGGTCCCCGA  
 ACCAGGAAGGGTTGAGGGAACACAATCTGCAAGGCCCGCGACCCAGGTGAGGGGGCCCGGTGTGGGTCTCTCC  
 TCCCTTTGACTTCCCAACCCCTCGGGCCCTTGGCTTTCTGGGGACCCCTCGCCGGGAGATGCGCCGGCTTGATG  
 CGGAGCAAGGATTCGTCTGCTGCTTGTCTACTGGCCGGGTGCTGATGGTGGAGAGCTCACAGATCGGCAGT  
 TCGCGGGCCAAACTCAACTCCATCAAGTCTCTCTGGCGGGGAGACGCCTGGTCAGGCCGCAATCGATCTGCG  
 GGCATCTGACCAAGGACTGGCATTCGGCGGCAGTAAGAAGGGGAAAAACCTTGGCGAGGCCCTACCCCTGTAGCAGT  
 GATAAGGAGTGTGAAGTTGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCCTGCATGGTGTGTGCGGAGA  
 AAAAAAGAGCGCTGCCACCGAGATGGCATGTCTGCCCCAGTACCCTGCAATAATGGCATCTGTATCCAGTTC  
 ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACACCGGTCAATTAC  
 TCAAAACATGACTTTGGGATGGCAGAACTAGGAAGACCACACACTAAGATGTACATATAAAGGGGATGAAGGA  
 GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTGTCTGTGCTCATCTTCTGGACAAAATCTGCAAAA  
 CCAGTGTCTCATCAGGGGGAAGTCTGTACCAAAACACGCAAGAGGGTTCTCATGGGCTGGAATTTTCCAGCGT  
 TGGCATGTGCGAAGGGCCGTGCTTGCAAAAGTATGGAAGATGCCACCTACTCCTCCAAAGCCAGACTCCATGTG  
 TGTGAGAAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTATTTAATGCATTATAG  
 CATGGTGGAAAATAAGGTTTCAGATGCAAGAAGTGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCAAAA  
 AAAGGGAGAAAGAAAACATGAACCTGAATAGATTAGAAATGGGTGACAAATGCAGTCGAGCCAGTGTTTCCATTATG  
 CAECTTGTCTATGTAAATAATGTACACATTTGTGGAATAATGCTATTATTAAGAGAACAAAGCACACAGTGGAAATT  
 ACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGGTTGTCTGGAGGAGAGGTTTCCCTCAGATTGCTGATTGC  
 TTATACAAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAAACAAAATACTCTAGAATAACTTTGTTA  
 TACAATAGGTTCTAAAAATAAAATGCTAAACAAAGAAATGAAACATGGAGCATTGTTAATTTACAACAGAAAAAT  
 TACCTTTTGATTGTAAACACTCTTCTGCTGTTCAATCAAGAGTCTTGGTAGATAAGAAAAAATCAGTCAATAT  
 TTCCAAAATAATTGCAAAAATAATGGCCAGTTGTTAGGAAGGCCCTTAGGAAGACAAATAAATAACAAACAAACAG  
 CCACAAAATACTTTTTTTTCAAAATTTTAGTTTTACCTGTAATTAATAAGAACTGTATCAAGAACAAAAACAGTTCC  
 TTCAGATTCTACGGAATGACAGTATATCTCTCTTATCCTATGTGATTCTGCTCTGAATGCATTATATTTTCCA  
 AACTATCCCATATAAATTGTGACTAGTATAAAATACTTACACAGAGCAGAAATTTACAGAGTGCAAAAAAATTTTAAA  
 GATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTTTCTTAAAGATTGGCCATAACCTATATTTT  
 GATAGAATTAGATTGTAATAACATGTATTACATACATACTCTGTGGTAATAGAGACTTAAAGCTGGATCTGTACTG  
 CACTGGAGTAAGCAAGAAAATTTGGGAAAACCTTTTTCGTTTGTTCAGGTTTGGCAACACATAGATCATATGTCTG  
 AGGCACAAGTTGGCTGCTTCACTTTTGAACACAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT  
 CATATAATTTACTATGCAGATGAATTCAGTGTGAGGTCTGTGTCGCTACTATCTTCAAAATTTATTTATTTATAG  
 TGCAGATCTCTCAATAATCTCAATTTACGGAGGTTTCAAAAAATGTACTCTGAAAGTAGACAGAGTAGTGAGG  
 TTTCAATGGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTTCTTCCCAAACTCTGCAGCATCTG  
 CTTTATTTGCCAAAGGGCTAGTTTCGGTTTTCTGCAGCCATTGCGGTTAAAAAATATAAGTAGGATAACTTTGTA  
 AACCTGCATATTGCTAATCTATAGACACCACAGTTTCTAAATTTCTTTGAAACCACTTTTACTACTTTTTTAAACTT  
 AACTCAGTTCTAAATACTTTTCTGGAGCACAAAACATAAAAGGTTATCTTATAGTCGTGACTTTTAAACTTTTG  
 TAGACACAATTCACCTTTTAGTTTTCTTTTACTTAAATCCCATCTGCAGTCTCAAAATTTAAGTTCTCCAGTAG  
 AGATTGAGTTTGGAGCTGTATATCTATTAAAAATTTCACTTCCACATATTTTACTTAAGATGATTAAAGACTTA  
 CATTTTCTGCAGAGTCTGCAAAAAACAAAATTTATAAATAGTCCATCCAAGAACCAAGTTTGTATAAACAGGT  
 TGCTATAAGCTTTGAAATGAAATGGAACATTTCAATCAACATTTCTATATAACAAATTTATATATTACAAT  
 TTGGTTTCTGCAATATTTTCTTATGTCCACCTTTTAAAAATTTATTTTGAAGTAATTTATTTACAGGAATG  
 TTAATTGAGATGATTTTCTTATAGAGATATTCTTACGAAGCTTTGTAGCAGATATATTTCGACATTTGTGAC  
 TTGTGAATTTAGGAAAAATGTATAATAAGATAAAATCTATTAAATTTTCTCTCTCAAAAACCTGAAAAA  
 AAAAAAAAAAAAAAAAAA

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## **FIGURE 42**

MAALMRSKDSSCCLLLLA AVL MVES SQIGSSRAKLNS IKSSLGGETPGQAANRSAGMYQGLA  
 FGGSKKGK NLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKKRCHRDGMCCPSTRC NN  
 GICIPVTESILTPHIPALDGT RHRDRNHGHYSN HDLGWQNLGRPHTKM SHIKGHEGDPCLRS  
 SDCIEGFCCARHF WTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS  
 SKARLHVCQKI

**Signal peptide:**

amino acids 1-25

## FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAAATCCACCTACCTTGGCCTCCCAAA  
 GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGCCAACATCACGTTTTTAAAAATTGATT  
 TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA  
 TAGTGCATTTATTTAGTCAGTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG  
 TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACTTG  
ATGTGTTTTAAAGCCTTGGGCAGAAATCTGTATTGTTGAGGATTGTTCCTTTTATCCCCCT  
 TTTAAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGACACCACAAAATGGCAAACA  
 TCACCAGCTCCCAGATTTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC  
 CCAAGTACACAGCAGAATAGTACAAGTCACCTACAACCTACTACTTCTTGGGACCTCAAGCC  
 CCCAACATCCCAGTCTCTCAGTCCTCAGTCATCTTGACTTCAAATCTAACCTGAGCCATCCC  
 CAGTCTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCAGTGTCTCTCT  
 CCTGGTTTGGAGTCCTTTCCTTCCCAGGCAAACTTCGAGAATCAACCTGGAGACAGCTGC  
 CTCCACTGTGAACAAGCTTTTGCAGCTTCCCAGCAGCACCATTGAAAATATCTCTGTGTCTG  
 TCCACCAGCCACAGCCCAAACACATCAAACCTGCTAAGCGGCGGATACCCCCAGCTTCTAAG  
 ATCCCAGCTTCTGCAGTGGAATGCCCTGGTTCAGCAGATGTCACAGGATTAATGTGCAGTT  
 TGGGGCTCTGGAATTTGGGTGAGAACCTTCTCTCTGAAATTTGGATCAGCTCCAAGCAGTG  
 AAAATAGTAATCAGATTCACATCAGCTTGTATTGCAAGTCTTTAAGTGAGCCTTTGAATACA  
 TCTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTCCGCTCATACCTCCTG  
 CAGTCTGACAAGCTCATCACTGAATCTGTGCTAGTCCAGTAGCAATGTCTTCTCTTATGACC  
 AGAGTTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA  
 GGAACCATCATGAATGGACATGGTGGTGGTGCAGTGCAGCAGACACTAGACAGTAAGTATAG  
 CAGCAAGCTACTCTTGTCTAGTGGCTGGTGCCAACCAAACAGAGGAAGAGGATAGCTCACGTGA  
 TGTGGAAAAACCCAGTTGGTCAATGGCTCATTTCGTTAAAGCAGCCCTTTTGCTTTTTTGT  
 TTTTGGACCAGTGTTGGCTGTGGTGTATTATAGAAATGTCTTAACCACAGCAAGAAGGAGGT  
 GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATACAGTATGCAT  
 TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCCATATCCCAGTGCTTTGGGGGGCC  
 AAGGCAGGCAGATTGCCAAAGCTCAGGAGTTTGAGACCACCCTGGGCAACATGGTGAACTC  
 TGCTCTACTAAATACGAAAAACTAGCCGGGTGTGGTGGCGGCGCGTGCCTGTAATCCCAG  
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC  
 GTCTGAAAAGA

# **FIGURE 44**

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT  
 PSTQQNSTSHPTTTTSSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPP  
 PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPPKHIKLAKRRIPPASK  
 IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT  
 SLSMTSAVQNSTYTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSESAP  
 GTIMNGHGGGRSQQTLDISKYSSKLLLSWLVPTKQRKRIAHVMWKTPVGQWLIR

**Signal peptide:**

amino acids 1-24

**FIGURE 45**

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCCATGGCGCTGCCATCCCGAATCCTGCT  
 TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG  
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCATACTGCCACCTCTACGAGAGCCTGGCC  
 GTCCGCCTGGAGGTACCGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA  
 GGTGCTGGCGGTGGCGCGCGCGCACCCGCTTCTGACCTGCGTGAACCGGGGACGTGT  
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGACTGGGACCGGCAGCCGCCGGG  
 GTCCCGCAGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCTA  
 CGGGCCCCCTTTTCTGCGGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT  
 TCTACTGCGTATCGAGCCGCTGGAGGTGCGCGACGAGGGCACCTACTCCTGCCACCTGCAC  
 CACCATTACTGTGGCCTGCACGAACGCCGCTCTTCCACCTGACGGTCGCCGAACCCACGC  
 GGAGCCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGCGCCCGAGGCCAG  
 ACCCCACACTGGCGCGCGGCCACAACGTATCAATGTATCGTCCCCGAGAGCCGAGCCAC  
 TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTTTCATCTGCTACTGGTCAC  
 TGTCTCTTGGCCGCCCGCAGGCGCCGCGAGGCTACGAATACTCGGAACGAGAAGTCGGGAA  
 AGTCAAAGGGGAAGGATGTTAACTTGGCGAGTTCGCTGTGGCTGCAGGGGACCAGATGCTT  
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAATCCTGAAGGAGAGGGCGGAGCT  
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCCGGAAGGAGAACT  
 GCAAATAGGGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC  
 CTCGGGGCATCTCCTGATGCTCCGGGGCTACCCCCCTTCCAGCGGCTGGTCCCGCTTTCT  
 GGAATTTGGCCTGGGCGTATGCAGAGCGCCCTCCACACCCCTCCCCAGGGGCTTGGTGGC  
 AGCATAGCCCCACCCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAACC  
 AAAATCCCCTGATGCCCATCATGCCCTCAGACCTTCTGGGCTCTGCCCGCTGGGGGCTG  
 AAGACATTCCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAATGGGGTCAGCCTCA  
 GGGCAGGAGTCCCCTCCTCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTTGAGGA  
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCGAGGATCCCACT  
 CCTCCTGGGGTGTGCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG  
 GCACCATCTGTTCTCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG  
 CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTTCTCTGCCCATCCCTACCCTAGCCTTG  
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCCTGACACCCCTCCCTT  
 GGACTCTGCTGGGCTGGAGTCTAGGGCTGGGGCTACATTGGGCTTCTGTACTGGCTGAGGA  
 CAGGGGAGGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTGCCACTCTCAGACCCACATTT  
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCATCTGATTTTTAAAAA  
 AAAAA

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## **FIGURE 46**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618

<subunit 1 of 1, 341 aa, 1 stop

<MW: 38070, pI: 6.88, NX(S/T): 1

MALPSRILLWKLVLLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTGPPAT  
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTDHRVEEAQQVVHWDRQPPGVPHDRADRLDL  
YASGERRAYGPLEFLRDRVAVGADAFERGDFSLRIEPLVADEGTYSCHLHHHYCGLHERRVF  
HLTVAEPHAEPPPRGSPGNGSSHGAPGPDPTLARGHNVINVIVPESRAHFFQQLGYVLATL  
LLFILLLVTVLLAARRRRGGYEYSQKSGKSGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN  
NILKERAELAHSPLPAKYIDLKGRKENCK

### **Important features:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domain:**

amino acids 237-262

#### **N-glycosylation site.**

amino acids 205-208

#### **Cell attachment sequence.**

amino acids 151-154

#### **Coproporphyrinogen III oxidase proteins.**

amino acids 115-140

**FIGURE 47**

CGCCGGAGGCAGCGGCGGCGTGGCGCAGCGGCAGC**ATG**GCCGTTGTCTCAGAGGACGACTTT  
 CAGCACAGTTCAAACCTCCACCTACGGAAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC  
 ACTGCTTGAGAAGCTGCTGGACCGCCCGCCCCCTGGCCTGCAGAGGCCGAGGACCGCTTCT  
 GTGGCACATACATCATCTTCTCAGCCTGGGCATTGGCAGTCTACTGCCATGGAACCTTCTTT  
 ATCACTGCCAAGGAGTACTGGATGTCAAACCTCCGCAACTCCTCCAGCCACGCCACCGGGGA  
 GGACCTTGAGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGCCGTTGCCTCCACCG  
 TGCCCTCCATGCTGTGCCTGGTGGCCAACCTTCTGCTTGTCAACAGGGTTGCAGTCCACATC  
 CGTGTCTGGCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACTGGTGAA  
 AGTGGACACTTCCCTCGGACCCGTGGTTTTTTTGGGTCACCATTTGCTGCATGGTGATCC  
 TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTCCATATG  
 AGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGCGGGACGGTCAGCGCCGTGCCTC  
 ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGG  
 CCACCATCTTCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCC  
 AGGTACTACATGAGGCCTGTTCTTGCGGCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCCA  
 GGACTCCCTCAGTGCCCTTCCGTGGCCTCCAGATTCAATTGATTTCCACACACCCCTCTCC  
 GCCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGCACCTACGTCTTCTTCATCAC  
 AGCCTCATCTACCCCGCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT  
 GTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCCCTCTGTACAACCTTTGCTGACCTAT  
 GTGGCCGGCAGCTCACCGCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCGCTCCCAGGG  
 TTCGTGCTCCTCCGGACCTGCCTCATCCCCCTCTTCGTGCTCTGTAACCTACAGCCCGCGT  
 CCACCTGAAGACTGTGCTCTTCCAGTCCGATGTGTACCCCGCACTCTCAGCTCCCTCTGG  
 GGCTCAGCAACGGCTACCTCAGCACCTTGGCCCTCCTCTACGGGCCTAAGATTGTGCCCAGG  
 GAGCTGGCTGAGGCCAGGGGAGTGATGCTCCTTTATGTGTGCTTGGGCTTAACACTGGG  
 CTCAGCCTGCTTACCCTCCTGGTGCACCTCATC**TAGA**AAGGGAGGACACAAGGACATTGGTG  
 CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCCATGGAGGAAAGGCC  
 TAAAGTTTCACTTGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCA  
 GTGAGCCACGTCCATGCCATTCCGTGCAAGGCAGATATTCCAGTCATATTAAACAGAACT  
 CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTCACAGCTGATGGTTA  
 ACATTTCCACCTTTCTTTAGCCCTTCAAAGATGCTGCCAGTGTTGCGCCTAGAGTTATTACA  
 AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCCAGCTGCGCTCATTCCAGCT  
 GACAGCGAGATGCAAGCAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGA  
 AGTCCCCTGCGATGGTCAGTCTCAGGCCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT  
 GCGGGTGAACAACCTGCCACTAACCAGACTGGAAGAACCCAGAAGATGGGCTTCCATGAAT  
 GCTTCATTCCAGAGGACAGAGGCCTCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG  
 TTTTCAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCTGGGTCAAGATGAGGGTC  
 TTTCACTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC  
 GTATTCAAAA

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**FIGURE 48**

MAVVS EDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGGLQRPEDRFCGTYIIFFSLGI  
GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL  
LVNRVAVHIRVLASLTVILAIFMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI  
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRSALAFFLTATIFLVLCMGly  
LLLSRLEYARYYMRPVLAHVFSGEEELPQDSL SAPSVASRFIDSHTPPLRPILKKTASLGF  
CVTYVFFITSLIYPVCTNIESLNKGSGSLWTTKFFIPLTFFLLYNFADLCGRQLTAWIQVP  
GPNSKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSLLGLSNGYLSTLAL  
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

**Transmembrane domain:**

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,  
305-330, 448-472



**FIGURE 49**

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCTGTGTGCACCAAGAGCTGGAGACACCA  
 TCTCCCACCGAGAGT**CATG**GGCCCCATTGGCCCTGCACCTCTCGTCTCGTCCCCATCCTCC  
 TCAGCCTGGTGGCTCCAGGACTGGAAGGCTGAACGCAGCCAAAGACCCCTTCGAGAAATGC  
 ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGGCTCAATCGGACCCCT  
 GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGGCTGGTGGCCGCCAAGGTGC  
 TCAGCGATGCTGGACACAAGGTCACCATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATC  
 TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCAG  
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCTGGGGCTCAACCTGACCAAGTTCACCC  
 AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG  
 AAGGTGCCCCGAGAAGCTGGGCTACGCCCTTGGCTCCCCAGGAAAAGGGCCACTCGCCGAAGA  
 CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGG  
 CGATGAAGAAGTTTGAAGGCACACGCTCTTGGAATATCTTCTCGGGGAGGGGAACCTGAGC  
 CGCCGGCGCGTTCGAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTT  
 CGCCGAGGCCCTCCGGGCCCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG  
 GTGGCTGGGACCTGCTGCCGCGCGCTGCTGAGCTCGCTGTCCGGGCTTGTGCTGTTGAAC  
 GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC  
 CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGTGCTGACGGCGAGCGGACCGG  
 CGGTGAAGCGCATCACCTTCTCGCGCCGCTGCCCGCCACATGCAGGAGGCGCTGCGGAGG  
 CTGCACTACGTGCCGCCACCAAGGTGTTCTTAAGCTTCCGCAAGGCCCTTCTGGCGCAGGA  
 GCACATTGAAGCGGCCACTCAAACACCGATCGCCCGTCGCGCATGATTTTCTACCCGCCGC  
 CGCGCGAGGGCGCGCTGCTGCTGGCCTCGTACACGTGGTCGGACGCGGCGCGAGCGTTGCC  
 GGCTTGAGCCGGGAAGAGGCGTTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC  
 TGTGCTGCGCCAGCTCTGGGACGGCACCGCGCTCGTCAAGCGTTGGGCGGAGGACCAAGCACA  
 GCGCCGGTGGCTTGTGGTACAGCCCGCGCTCTGGCAAACCGAAAAGGATGACTGGACG  
 GTCCCTTATGGCCGCATCTACTTTGCCGGCGAGCACACCGCCTACCCGCACGGCTGGGTGGA  
 GACGGCGGTCAAGTCGGCGCTGCGCGCGCCATCAAGATCAACAGCCGGAAGGGGCTGCAT  
 CGGACACGGCCAGCCCCAGGGGCACGCATCTGACATGGAGGGGCAGGGGCATGTGCATGGG  
 GTGGCCAGCAGCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCTCCAGTCCAAGG  
 CCAGTTATCTCTCCAAAACAGACCCACACAGGACCTCGCAT**TAA**AGTATTTTCGGA AAAA  
 AA

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**FIGURE 50**

MAPLALHLLVLPILLSLVSQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQRV  
IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIL  
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLGALRPQEKGHSPEDIYQMA  
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLDVMSSEDGFFYLSFAEALR  
AHSCSLDRLQYSRIVGGWDLPRALLSSLSGLVLLNAPVVAMTQGPVDVHVQIETSPPARNL  
KVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEGG  
HSNTDRPSRMIFYPPPREGALLASYTWSDAFAAGLSREEALRLALDDVAALHGPVVRQL  
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS  
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGQLSLQ  
NTTHTRTSH

**Signal peptide:**

amino acids 1-21

**FIGURE 51**

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCGGGCCTCTGCCTGCA~~T~~  
 GGACGCTCTGAAGCCACCCCTGTCTCTGGAGGAACACAGAGCAGGGGAAGAGGACAGGACTCGTGTGGCAGGAA  
 GAACTCAGAGCCGGGAAGCCCCCATTCACTAGAAAGCACTGAGAGATGCGGCCCCCTCGCAGGCTCTGAATTTGCT  
 GCTGCTGTTTCACAAGATGCTTTTTATCTTTAACTTTTTGTGTTTTCCCACTCTCCGACCCCGGCGTGTATCTGCAT  
 CTTGACATTTGGAGCTGCCATCTTCTGTGGCTGATCACCAGACCTCAACCCGCTTTACCTTTCTTTGACCTGAA  
 CAATCAGTCTGTGGGAATTGAGGAGGAGCAGCGAAGGGGGTTTCCCAAGAAACAAATGACCTAACAAAGTTGCTG  
 CTTCTCAGATGCCAAGACTGATGTAGGTTTCCAAAGAGGACTCGCTGTCTGACAATGGGCCCTGTGTGGG  
 ATATAGAAAACCAACAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGCAGAGTACCTGGGTTT  
 CTGCTCTTGCATAAAGGTTATAAATCATCACCAGACCGATTGTGCGGCATCTTTGCTCAGAATAGGCCAGAGTG  
 GATCATCTCCGAATTGGCTTGTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTTGGGACCAGAAGC  
 CATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACATGCCAAAGGCATTTGGTGCTGAT  
 AGGGAATGTAGAGAAAGGCTTACCCCGAGCCTGAAGGTGATCATCCTTATGGAACCCCTTTGATGATGACCTGAA  
 GCAAAGAGGGGAGAAGAGTGGAAATTGAGATCTTATCCCTATATGATGCTGAGAACCATAGGCAAAAGACACTTCAG  
 AAAACCTGTGCCTCCTAGCCAGAAAGACTGAGCGTCATCTGCTTACCAGTGGGACCACAGGTGACCCCAAAGG  
 AGCCATGATAACCCATCAAAATATTGTTTCAAATGCTGCTGCCTTCTCAAATGTGTGGAGCATGCTTATGAGCC  
 CACTCCTGATGATGTGGCCATATCCTACCTCCCTCTGGCTCATATGTTTGAAGGATTTGACAGGCTGTTTGTGTA  
 CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTGCGTTGCTGGCTGACGACATGAAGACTTTGAAGCC  
 CACATTGTTTCCCGCGGTGCCTCGACTCCTTAAACAGGATCTACGATAAGGTACAAATGAGGCCAAGACACCCCTT  
 GAAGAAGTTCTTGTTGAAGCTGGCTGTTTCCAGTAATTTCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG  
 TTTCTGGGACAAGCTCATCTTTGCAAAAGATCCAGGACAGCCTTGGGCGGAAGGGTTGCTGTAATTGTCACTGGAGC  
 TGCCCCATGTCCACTTCAGTCACTGACATTTCTTCCGGCGACCAATGGGATGTCAGGTGTATGAAGCTTATGTTCA  
 AACAGAAATGCACAGGTGGCTGTACATTTACATTACCTGGGGAAGTGGACATCAGGTACAGTTGGGGTCCCTTGGC  
 TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAACCTACTTTACAGTGAATTAAGGAGAGAGGTCTGCAT  
 CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCTGAGAAGACAGGAAGCCCTGGACAGTGATGGCTG  
 GCTTCACACAGGAGACATTGGTCTGGCTCCGCAATGGAACCTCTGAAGATCTGACAGCTAAAGGCACTTTT  
 CAAGCTGGCCCAAGGAGAATACATTGCACCAGAGAAGATAGAAAATATCTACACACAGGAGTCAACCAAGTCTTACA  
 AATTTTTGTACAGGGGAGAGCTTACGGTCACTCTTAGAGAGTGGTGGTCTCTGACACAGTCAAGCCATTTTCCCTC  
 ATTTGACGCCAAGCTTGGGTTGAAGGGCTCCTTTGAGGAACCTGTGCCAAACCAAGTGTGAAGGAAGGCCATTT  
 AGAAGACTTGCAGAAAATTTGGGAAAGAAAGTGGCCTTAAACCTTTGAACAGTCAAGGCACTTTTCCCTATCC  
 AGAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTTGAAGCAAGCGAGGAGACTTCCCAATACTT  
 TCGGACCCAAATGACAGCCTGTATGACACATCCAGGATTAGGATAAGGTACTTAAGTACCTTCCCGGCCCACTG  
 TGCACTGCTTGTGAGAAAATGGATTAAAACTATTCTTACATTTGTTTGCCTTTCCCTCTATTTTTTTTTAAAC  
 TGTTTAACTCTAAAGCCATAGCTTTTGTTTATATTAGACATATAATGTGTAACCTTAGTTCCCAATAAATCA  
 ATCCGTGTTTCCCACTCTCGATGTGCTAATATTAAGGCTTCAGGGCTACTTTTATCAACATGCCTGTCTTCAA  
 GATCCAGTCTTATTGTTCTGTGTCCTTCTCATGATTTCCAACCTTAATACTTATGTAACCAACAGTTCAAGGT  
 CAAAGGACCCCTCTGTGCCTTCTTCTTTGTTTGTGATAAACATAACTTCCCAACAGTCTCTATGCTTATTATACA  
 TCTTCTTACTGTTTCAAACCTAAGAGATTTTAAATCTGAAAAACGCTTACCAATTCATGTTTCTTAAAGCAATTTA  
 AAACCACTAAAAATTTAGTTTTCAGCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCGGATGCTCTT  
 TCGCTGAAATTTAAATTTGTACTGTACTGAGGAAAGTTTGTATCATACCAACATTTCTCAATCTCTGATGTAGATA  
 CTCGACTTGGGAGTATTTAAATTTGGGCTATGACATACTGTCCAAAGCAATGTGCTTCTTAAAGCAATTTA  
 CAGTAGGAACCTGGGAGTAACTCTGTCCTTCCCTACAGTTTGTCTGAGCTGGAAGCTGTGGGGAGAGGATGACA  
 GGTGGGCCAGTGAACCTTTCCAGTAAATGAAGCAAGCACTGAATAAAACCTCTGTAACCTGGGAACAAAGATCT  
 ACAGGCAAGAAATGCCACACACAGGCTTATTTCTGTGAAGGAACCACTGATCTCCCCACCCCTTGGATT  
 AGAGTTCCTGCTTACCTTACCCACAGATAACACATGTTGTTTCTACTGTAAATGTAAAGTCTTTAAATAAAC  
 TATTACAGATAAAAA

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## **FIGURE 52**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775
<subunit 1 of 1, 739 aa, 1 stop
<MW: 82263, pI: 7.55, NX(S/T): 3
MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFN
FLFSPLPTPALICILTFGAAIFLWLITRPQPVLPLDLNNQSVGIEGGARKGVSQKNNDLTS
CCFSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS
PDQFVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTFPQKAL
VLIGNVEKGFTPSLKVIIIMDPFDDDLKQRGEKSGIEILSLYDAENLKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIVSNAAFLKCV E HAYEPTPDDVAISYLP LAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPVAVPRLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFELQKGIIRHDSFWDKLIFAKIQDSLGGRRVRVIVTGAAPMSTSVMTFFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTSGHVGVP LACNYVKLEADVADMYFTVNNEGEVCIKGTNVFK
GYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR
SQPVLQIFVHGESLRSSLVGVVVPD TDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPF SIENGLLTPTLKA KRGELSKYFRTQIDSLYEHIQD
```

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 61-80

#### **Putative AMP-binding domain signature.**

amino acids 314-325

#### **N-glycosylation site.**

amino acids 102-105, 588-591 and 619-622

GGAGCGCGAGGCCGCGCGAGACCGGGCCGAGCAGTGAAGGCCCTAGCGGGGCCGAGCGGGG  
 CCCGGTGGCGCCCTAAGCATCTCTGAAGTCATGGGCTGGCCAGGACATTTGGTGACCGCCCAAT  
 CCGGTATGCGAGCTGGAAGGAGCCGCCCTCATCAAGCCCTTTGGGGCTCGGAAGAACGCG  
 AGCTGGTACTTCTTACTGGAAGTATAAATGACAACACGCGGCCCTCGGAGATTCTGTCTCA  
 GACAGGGGCCGTGCTTTTCTGCTGGTGACTGTCATTGCAATCAAGTGTATCTCTGGACA  
 CTCGGCGAGCCATCAGTGAAGCCATGAAGACCCAGAGCCAGGACAGCAAGCATGATGAGGCC  
 CTAGGCGCGCTGAGCGCCCCAGGCGCGAGGCGAGTGGTCCCGCGGGTCTCGGACGCTAGA  
 GGTGTATTCAAGTCGCAAGCATATATGTGGCAGTGATGCACACCGTGTCTGGAGAT  
 AGGCGCGGAGGACGAGGCGGGGGCATCTATGTCTATTGTCTCAACAGGCCACGGGCCACGTG  
 ATGGCAAAACGCTGTTTGACACGCTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCTT  
 CAACATGGTAGCGCGCGCGGAGTGCTCATCTGCCACTGTCAAGGATGAGGCTCCTTCACC  
 TCAAGGACACAGCCAAAGGCTCTGCTGAGAGCGCTGGGACGAGCGCTGGCCCTGCCCTGGG  
 TGGAGGACACATGGGCTTCGTGGGACGAAAGGAGTGCTGTCTCTCGGGGAGAACATTC  
 TAAGTCACTTGCCTCTCTTCTTGGGGGACCCAGTCTGTCTGAAGACAGATGTGCCATTGA  
 GCTCAGCAGAAGAGGCGAGAGTGCCATGGGCGAGACACAGAGCTGAACCTCTCGCCGCGGCG  
 TTCTGACGAAAGTTGGGGCTATGGAAGTGATGTCAGCTGCAAGGACCCACACCCATCTGA  
 GTACGCCCTGACCCATCCGACACAAAGGTCTCAATGTGCCGTGGGTGTCAATTGACG  
 GAAACGCCCACTAATCTGTATACAGATGCTGGCTCTCTGTTCTAGCCAGGGGTGTCT  
 CCTCAGATGATAACAGTTTTTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGCCACT  
 GTTGGTCTGAGGGGACCATCAGCACTACTCCCATCAGCATCAAGAAATCGCCGGTGTCTCAGC  
 ACTACAAGGCCAGGCTCAGTGCCACTTCAACCTGTGTTCCGAGGCCAAGTTTGTGTGGTT  
 CTGGAAGGAGGACCTGGACATGTCTGTGATTTTTTCAGTTTCTGAGCCAACTCATCTCAAC  
 CTTGAGGAGGATGACAGCCTTGCTGGACTCTCTGCTGGAATGACCAGGGGTATGAACACA  
 CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCTGGGCTGGGCTGGGTGCTC  
 AGGAGGTCTCTTGACAAGGAGGAGCTTGAGCCCAAGTGGCTTACACGGAAAGCTCTGGGA  
 TTGGGACATGTGGATGCGGATGCTTGAAACAACCGCGGGCGAGAGTGATCATCTCTGAGC  
 TTTCCGATCTTACCATTGTCATCTGTCGGCCTCAACATGAATGGCTACTTTACAGAGGCC  
 TACTTTCAAGAAGACAAGTTCAACACGGTTTCAGGTGTCAGCTCAGGAATGTGGACAGTCT  
 GAAGAAAGAAGCTTATGAAGTGGAGTTACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC  
 ACAGCAAGAAGCCCTTGTAAGACTCTTTCTCGCAGACACAGAGGGCCACACCTCATGCTGGC  
 TTTATTCTGAATGGGAAGATGATGACTTCAACACTTGAGCCAGCTTGGCAAGTGCCTCCA  
 TATCTGGGACCTGGATGTGCTGTGCAACCATCGGGGCTGTGGAGATTGTTTCGGAAGAGA  
 ACCATTCTCTGTGTGGGGTCCCGGCTTCCCGCTCAGTGAAGAAGCCACCCCTCAGT  
 ACCCAATTTTCTGAGACACCCCAAGGAGGAGGAGGCCAGGAGCCCAAGAACAGAC  
 ATGAGACCTCTCCTGAGAGCCTCGGGGCTGGGTATGTGTAACCCCAAGCTGCTGATGCC  
 TCCCTCCATCTGTAGGATTTTGTAGATGCTGTGAGGGCTGGGCTACTTGTGTTTAA  
 TGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCCGTGTCTCAACACCCCGTCTCTGAGTT  
 AAAAGTCTATTATTATCTCTTGTGGAGAGGGCAGGAGAGTACCTGGGAATCATTA  
 ATCTCTAGACGCTACTCTGCCCTTTGAATACCTCATGTTCCAGGCTGGCTCAGAACTTA  
 ACTTATTATTAGACTGCTCTGAGGCGCTTGAANAACAGGCCGAACCTTGGAGGGCTGGAATT  
 TTTTGGGCTGGAATGCTGCCCTGAGGTTGGGCTGGCTTACTCAGGAACCTGCTGTGCC  
 CAACCCATGGACAGAGCCAGCTGGGGGCCACATGCTGACACAGACTCACTCAGAGACCCCTTA  
 GACACTGGACAGGCCCTCTCTCAGCCTTCTGTTTGTTCAGATTTTCAAGCTGGATAGTT  
 GGTCACTGATTAAAAAAGGAGAAGCCCTCGGAAAAAATAAAAAAATAAAAAA

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## **FIGURE 54**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQRALRRFCQTGAVLFLLVTIVNIKLILDTR
RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEA
REQGRGIHVIVLNQATGHVMAKRVEDTYSPEHEAMVFLNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNRRRRRRFCSKVEGYGSVCCKDPTPIEFSPDPLPDKNVNLNVPVAVIAGN
RPNLYRMLRSLLSAQGVSPQMITVFIDGYEEPMDDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPFAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRRLSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLSLKEAYEVEVHRLLEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDDFTTWTQLAKCLHIWDLVDVRGNHRLWRLFRKKNH
FLVVGVPASPSYVKKPPSVTPIFLEPPPKKEGAPGAPEQT
```

**Important features of the protein:**

**Transmembrane domain:**

amino acids 38-55

**Homologous region to Mouse GNT1**

amino acids 229-660

**FIGURE 55**

CGGACGCGTGGGCTGCTGGTGGGAAGGCCCTAAAGAACTGGAAGGCCACTCTCTTGGAACCACCACAC  
 CTGTTTAAAGAACTTAAGCACCATTAAAGCCACTGGAAATTTGTTGCTAGTGGTTGTGGGTGAATA  
 AAGGGGGCAGAAATGCATGATTTCATCTCCATTAGCCTGCTGCTCTGCGTATGTTGGTGGGATGTTA  
 CGTGGGCGCAATCATTCCTTGCGTGTAAATTTCTCAGAGGAACGACTGAAGCTGGTGACTGTTTGG  
 GTGCTGGCCCTTCTCTGGAACGTCTCTGGCAGTCATCGTGCCTGAAGGATGCATGACCCCTTATGAA  
 GATATTCTTGAGGGAAAAACACCCAAAGCAAGTGAACACATAATGTGATTCATCAGACAAAGCAGC  
 AGAAAAATCAGTTGTCCATGAACATGAGCACAGCCACGACCACACACAGCTGCATGCCATATTGGTG  
 TTTCCCTCGTTCTGGGCTTCGTTTCATGTTGCTGGTGGACAGATTGGTAACCTCCCATGTGCATTCT  
 ACTGACGATCCGAAGCAGCAAGGTCTAGCAATTCAAAATCACCACCAGCTGGGTCTGGTGTGCGA  
 TGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGACAGTGTCCAGTTAATTG  
 TGTTTGTGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCCCTTCTTGATGCTAGCT  
 GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCAT  
 GGTGACATACCTTAGGACTGAGTAAGAGCAGTAAGAAGCCCTTCAGAGGTGAACGCCACGGGAGTGG  
 CCATGCTTTTCTCTGCCGGGACATTTCTTTATGTTGCCACAGTACATGCTCCTCCTGAGGTGGGCGGA  
 ATAGGCGCAGGCCACAAGCCCGATGCCACGGGAGGGAGAGGCCCTCAGCCGCTGGAAAGTGGCAGCCCT  
 GGTTCGTGGGTTGCCCTCATCCCTCTCATCTGTGTCAGTAGGACACGAGCATTAAATGTTCAAGGTCCAGC  
 TCTGGTCCAGGGCCGTTTGGCATCTCAGTGAGAACAGCCGGCAGCTGACAGCTACTCAGTCTCCTCAGT  
 TCTTGCTCACCTTGGCAGCTCTCTACATGTATTCTTAGAGTCCAGAGGGGAGGTGAGGTTAAACCTG  
 AGTAATGGAAAAGCTTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTATAGACATCCCATTGTGT  
 TATCTTTTAAAGGCCCTTGACATTTTGGCTTTTAATATTTCTTAAACCTATTCTCAGGGAAGATG  
 GAATTTAGTTTAAAGAAAAGAGGAGAACTTCATACTCACAATGAAATAGTGATTATGAAATACAGT  
 GTTCTGTAATTAAGCTATGTCTCTTTCTTTAGTTTAGAGGCTCTGCTACTTTATCCATTGATTTT  
 AACATGGTTCCCACCATGTAGAGCTGGTGTCTTAGCATCTATGCCACATGCGTTGATGGAAGGTGATA  
 GCACCACTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGCTCAGGAAAATGATAGC  
 AAGACACATTTGAAAGCTCTCTTTATACTCAAAAGAGATATCCATTGAAAAGGGATGCTAGAGGGATT  
 TAAACAGCTCCTTTGGCAGCTGCCCTCTCGAATCCAGCCTGCCATTCATCAATGGAGCAGGAGAGG  
 TGGGAGGAGCTTCAAAGAGGTGACIGGTATTTTGTAGCATTCCCTGTCAAGTTCTCCTTTGCAGAAT  
 ACCTGTCTCCACATTCCTAGAGAGGAGCCAAAGTTCTAGTAGTTTCAGTTCTAGGCTTTCCTTCAAGAA  
 CAGTCAGATCACAAGGTGCTTTTGGAAATTAAGGGATATTAAATTTTAAAGTGATTTTGGATGGTTAT  
 TGATATCTTTGTAGTAGCTTTTTTAAAGACTACCAAAATGTATGGTTGTCCTTTTTTTTGTTTTT  
 TTTTTTTTAATTATTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGGTCAAGCTTT  
 GGCACACTGTGTCTTCTCAATAAACCACCTGTAGCAAGATGGATCAATAAGAGAAGTGTTTGCCATA  
 TTGATTTAAAGCTTATTGGAATCATGTCTCTGTCTCTTCTGCTTTTTCTTGCTTTCTTCAACTTT  
 TCCTCTAGCCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTTAAATATTGTGTGGGATGAATT  
 CTTATCAGGACAAACCATTCTCGAAGTGAATAATGAAGATAATAATATCTTTATCTTTATCCCTT  
 CRAAGAAATTAACCTTTGTGTCAATGCGCTTTTGTGACCCCTTAAATACCACTCCTCATGTGTAA  
 ATTGACACAACTCACTAATCTGGTAATTTAAACAAATGAGATAGCAAAAGTGTTTAAACAGACTAGGATA  
 ATTTTTTTTCATATTTGCCAAAATTTTGTAAACCTGTCTGTGCAAAATAGTGATATAATTTGTAT  
 TATTAATTTATTTTACTTTCTATACCAATTTCAAAACACATTACCTAAGGGGGAAACCAAGACTAGTT  
 TCTTCAGGGCAGTGACGTAGTAGTTTGTAAAAACGTTTTCTATGACGCATAGCTAGCATGCCATATG  
 ATTTATTTCTCTCATGAATTTGTCACTGGATCAGCAGCTGTGGAATAAAGCTTGTGAGCCCTCTGCT  
 GGCCAGTGGAGGAAGTAGCAAAATAGGATACAGTTGTATGTAGTCTTGCAACAAATTGATACACA  
 ATTTTACTACCAAGAGAAGGTATAGTATGGAAGTCCAAATGACTTCCTTGATTGGATGTTAACAGCT  
 GACTGGTGTGAGACTTGAGGTTTCATCTAGTCCTTCAAACTATATGGTTGCCTAGATTCTCTCGGA  
 AACTGACTTTGTCAAATAAATAGCAGATTGATGTCAAAAAA

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**FIGURE 56**

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL  
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMILLVDQ  
IGNSHVHSTDDPEAARSSNSKITTTLGLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK  
APAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML  
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILLSVGHQH

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 37-56, 106-122, 211-230, 240-260, 288-304



GCTCGAGGCCGGCGCGCGCGGGAGAGCGACCCGGGCGGCTCGTAGCGGGGCCCGGATCCC  
CGAGTGGCGCGCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG  
GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGCCTGCATC  
ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCAGACACGGAT  
CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGCGGCCCTGGAGCTGAAGA  
AGAACGAGTTCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC  
CACAACCTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTGGTGAA  
TAACATCACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGA  
GGAATTACGGCAGGCTGCACGAGGATGTCTCCAGTTCTCAGAAAGACGACCAACCTGGAG  
AGGAAGTTCTCTACGACTGAGCCAGTGCATCAATCAGATGAAGAGGCTGAAGGAACACTG  
TGAGGAGCGAATAGAAGAGGTTACCAAAAAGGGGAATGAAGCTGTAGCTTCAGAGACCTGA  
GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCAGGCTGCAG  
GCAGCAGGCTGCCACACACAGAGGTGCCACAAGGGAAGGGAACAGTTGGTAAACAGCAA  
GTCCAGACACCAGCCCCAGTTCGGAAGTGTTTTGGATTCAAAGAGACAAGTTGAGAAAG  
AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGAGGAG  
CCAGGCCGGGAGCAGGTGGTGGGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG  
AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCACTGAGCCAGGAAAATCCAGAGA  
TGGAGGGCCCTGAGCGAGACCAGCTTGTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT  
GCCGGGGAAGGGAGAAACCAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA  
TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG  
TTTTTAATGTTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCTG  
ATAATACACTCTGAATTGAACTGGAATCACATATTTCACTACAGGCGCGAAGAGTACTGA  
TAAATTTTCTTACGAGGACTGAATCTGAAACTGTGAAATGTACTAAATGAAATGTACATCTG

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## **FIGURE 58**

MMGLNGRRSMKSPPLVLAALVACIIVLGFNYWIIASSRSVDLQTRIMELEGRVRRAAAERGA  
VELKKNEFQGELEKQREQLDKIQSSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL  
KTLQRNYGRLLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA  
SRDLSNNNDQRQQLQALSEPQPRLQAAGLPHTVEVPQGKGNVLGNSKSQTAPSSSEVVLDSKR  
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQ  
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQLRGEDDYNMDENEAESETDKQAALAGND  
RNIDVFNVEDQKRDTINLLDQREKRNHTL

**Signal peptide:**

amino acids 1-29

**FIGURE 59**

GGATG CAGAAAGCCTCAGTGTGGCTCTTCCTGGCCTGGGTCTGCTTCCTCTTCACTACGCTGGCATTGCCCTCTTCA  
 CCAGTGGCTTCTCTGCTCACCCTGTTGGAGCTCACCACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTGCC  
 TGCCATGGGGGAGCCAAAGGGAACCTGGGGCTCTGGATGGCTTCCCGATTTTCGCGGGTTGTGTTGGTGCTGA  
 TAGATGCTCTGCGATTGTACTTCGCCAGCCCCAGCATTACACAGTGCTAGAGAGCCTCCTGTCTCCCTACCTCT  
 TCCTGGGCAAACTAAGCTCCTTGCAGAGGATCTGGAGATTACAGCCCCACCATGCCCGCTCTACCCAGTCTCAGG  
 TGTACCTCTACCAACCACATGTCAGCGCTCAAGGCCCTCACCCTGGCTCACTGCCTACCTTATTGATGCTG  
 TAGTAACCTTCGCCAGCCAGCCATAGTGGAAAGACAATCTATTAGCAGCTCACCAGTGGAGGAGGCGGTAG  
 TCTTCATGGGAGATGATACCTGGAAGACCTTTTCCTGGTGCTTTCTCCAAAGCTTCTTCTTCCCATCCTTCA  
 ATGTCAGAGACCTAGACACAGTGGACAATGGCATCTGGAACACCTCTACCCACCATGGACAGTGGTGAATGGG  
 ACGTGCTGATTGCTCACTTCCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTCACCACCTGAAATGGGCCA  
 AGAACTTAGCCAGATGGACAGGTGATCCAGGACTTGTGGAGCTGTGGAGAATTGACACATGCTGGTAGTGG  
 CTGGGACCATTGGGATGACCACAAATGGAGACCATGGAGGGGACAGTAGCTGGAGGTCTCAGTGTCTCTTTC  
 TGTATAGCCCCACAGCAGTCTTCCCGACACCCACAGGAGGACAGAGGTGATTCTCAAGTTAGCCTTGTGC  
 CCACGCTGGCCTGCTGCTGGGCTGCCCATCCATTGGGAATATCGGGGAAGTGATGGCTGAGCTATTCTCAG  
 GGGGTGAGGACTCCACGCCCACTCCTCTGCTTTAGCCCAAGCCTCAGCTTCCCATCTCAATGCTCAGCAGGTGT  
 CCGGATTTCTTCATACCTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTCT  
 TCTCCAAGGCTCTGCTGACTACCAAGTGGCTTCTCAGAGCCCCAAGGGGCTGAGGCGACATGCCGACTGTGA  
 TTGCTGAGCTGCAGCAGCTTCTCGCGGGGAGCTCGGGCCATGTGCATCGATGTCTGGGCTCGTTTCTCTCTGGTCC  
 GCATCGCGGGGGTACTGCTCTTCTTGGCTGCTTCTGCTTTATCTGCTGCTGGCATCTCAGTGGGCAATATCCC  
 CAGGCTTTCCATTCTGCCCTCTACTCTTGACACCTCTGGCCTGGGGCTCGGTGGGGCCATAGCGTATGCTGGAC  
 TCTCTGGAACTATTGAGCTGAAGCTAGATCTAGTGCTTCTAGGGGCTTGGCTGCAGTGAGCTCATTTCCCTCTT  
 TTCTGTGGAAGCCTGGGCTGCTGGGGGTCCAGAGGGCCCCGTGGCAACCTCTGTTCCCATCCCTGGGCCCTGCTC  
 GTTTACTCTGCTCTTTTTCGTTGGGTGTGTTCTTCTCTGATAGTTTTGTTGATGCTGAGGCGAGGGCCACCCCT  
 TCCTTTTGGGCTCATTTACTCTGCTTGGTGTGTCAGCTTCACTGGGAGGGCGAGCTGCTTCCACTAAGCTAC  
 TCACAATGCCCGGCTTGGCATCTCAGCCACAACACCCCAAGGCAATGGCATATGCCGTAGCCCTGAGCTG  
 GAATTTGGGTGCTTTTATGTACAAGGCTAGCTGGGCTTTTCATCGTTGCCCTGAAGAGACACTGTTGGCACT  
 CCTCTCCGCTGCTGAGTCTCTTGACCATCATGGTGGTGGTGGTGGAGCCAGAATTTATGATTTGAGCTTGTGGTGG  
 CGCGCTCGTGGCCCTGTAGCTGCCGTGCGCTTGTGGCTTCGCGCTATGTTAATCTCAAGAGCCCGGACAC  
 CCATGCTCTTTGTGCGCTGGGACTGCCCTAATGGCATGGGTACTGCTGCCATCTGGGCATGGCGCTCGGGG  
 CAGATGAGGCTCCCCCGCTCTCGGGTCTGGTCTCTGGGCACTCATGGTGCTGCTCGGGCTGTAGCAGGGC  
 TGCTGCTTTCAGGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACAGTCTGGTGAAGGCTGGGGAGCGCCTCAA  
 GGACAGGACTGTCTCACTCCTCTCTCAGGCCCCCCACTTCTCAAGCTGACTGGATTATGTGGTCCCTCAA  
 TCTACCGACACATGCAGGAGGAGTTCCGGGCGGGTTAGAGAGGACCAAACTCAGGGGTCCCCTGACTGTGGCTG  
 CTTATCAGTTGGGAGTGCTACTCAGCTGCTATGTTCAAGCCCTCAGCCTGTGGCCTTCCCACTTCTGCTGT  
 TGATCGGAGGAGTCACTGAGCTTGTGTTCTGCTTCTGTTCTGCAGAGCTTCTTCTCAATCTGCTTGTGCTG  
 CTGGGATACCGCTCACCACCCCTGGTCTTTACTGTGCCATGGCAGGAGCTCTGGCTTGGGCCCTCATGGCCA  
 CACAGACTTCTACTCACAGGCAACAGCTGTCTTCAGGCCATCCATTGGCATGTGAGCTTCGTGGGATTCC  
 CAGAGGTTCACTGGCTCTGACTTGGCTGCTGCTTGTGATGGGAGCCAAACCTTTGGCTCCCACCTCTCTCT  
 TTGCACTAGGTTGCCACTCTGCTGCTCTGCGCTTCTGTTGTGAGAGTCAAGGCTGGGAGAGACAGCAGC  
 CCCCAGGAAATGAGCTGATGCCAGAGTCAGACCCGAGGAGGAGAGGAGGACCTGATGAGATCGCGCTTCGCG  
 ATGCGCTCAGCACTCTATGCAGCACTGCTGCAGCTGGGCTCAAGTACCTCTTTATCCTTGGATTCAAGATT  
 TGGCCTTGGCTTGGCAGCTCCATCCTTCGACAGCATCTCATGCTTGGAAAGTTTGGCCCTAAGTTCAAT  
 TTAGGCTGTGGGCTCATGTGAGCAGCGTGGGACTTCTCTGGCATGCTTGGTGATGAGAGTGGATGGTG  
 CTGTGAGCTCTGCTCAGCAGCTATTCTTGGCCAGCAGAGGCTAGCTAGTCTGTGATTACTGGCACTTGGCT  
 ACAGAGAGTGTGGAGACAGTGTAGCTGGCTGTGACAGTACTGGATGATCTGCAAGCAGGCTCAGCCATAC  
 TCTTACTATCATGCAGCCAGGGCGGCTGCATCTAGGACTCATATTCTATATATCAGGACACAGTGGAGTA  
 TGATCCCTTACTCTGATTGTGGATGCATCTGAGGACAGAGGGGGCGGCTCTCGGAGTGAATAAATAGGCGCG  
 GCGTGGTGACTGCACCTAATATCCAGCACTTGGGAGGACAGAGTGGGAGGATGCTTGGTCCAGGAGTTCA  
 AGACCAAGCCTGTGGAACTAAACAGACCCGCTCTCTACTATTTAAAAAAGTGTAATAAATGATAATAT

## FIGURE 60

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809

<subunit 1 of 1, 1089 aa, 1 stop

<MW: 118699, pI: 8.49, NX(S/T): 2

MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPGPGSLPWGSQGKPGACW  
MASRFSRVVLVLIDALRFDAQPQSHVPREPPVSLPFLGKLSLQRILEIQPHHARLYRSQ  
VDPPTTTMQRLKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMDGDTWKDLF  
PGAFSKAFFPFSFNVRLDLDVDNGILEHLYPTMDSGEWDVLIHFLGVDHCGHKHGHHPHPEM  
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGTTNGDHGGDSELEVSALFLYSPTAVFPST  
PPEEPEVIPQVSLVPTLALLLGLPIPFNGIVEVMAELFSGGEDSQPHSSALAQASALHLNAQ  
QVSRFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG  
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAIISPGFFPCPLLLTPVAWGLVGAIA  
YAGLLGTIELKLDLVLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPIPGPVLLLLLFRLA  
VFFSDSFVVAEARATPGLLGSFILLVVLVQLHWEGQLLPKLLTMPRLGTSATNPPRHNGAY  
ALRLGIGILLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA  
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPRLRLVIVSGASMLVP  
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE  
EFRGRLERTKSQGPLTVAAYQLGSVYSAMVTALTLLAFPLLLLHAERISLVFLLFLQSFL  
LLHLLAAGIPVTPPGPFTVPWQAVSAWALMATQTFTYSTGHQPVFPAIHWHAAFVGFPEGHGS  
CTWLPALIVGANTFASHLLFAVGCPLLLLLWPLFCESQGLRKRQPPGNEADARVRPEEEEEEP  
LMEMRLRDAPQHFYAALLQLGLKYLFIILGIQILACALAASILRRHLMVWVKVFAPKFIIFEAVG  
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

### Important features:

#### Signal peptide:

amino acids 1-16

#### Transmembrane domains:

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,  
1016-1034, 1052-1070

#### Leucine zipper pattern.

amino acids 843-864

#### N-glycosylation sites.

amino acids 37-40, 268-271

**FIGURE 61**

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGCGCCTTGGGGACGGGCAGTTCCCTGT  
 GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGA**AATGT**  
 CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT  
 TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTGTGT  
 CCTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAA  
 TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC  
 CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT  
 ACACGTGGAGTCCTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG  
 CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAATCATCTTCTGGTATGTTTTG  
 CCCATATCTATTACCGTGTTCCTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA  
 CGTTGGCAAAGAGAAACACCCAGCAAAATTTGATTTTGATTATGGAATGAATTTGACAAA  
 GATTCTTTGTGCCTGCTGAAAAAATCGTGATTAACCTTATCACCCCTCAATATCTCGGATGAT  
 TCTAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAA  
 TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG  
 GGTATGCTTCGCATTTGATGGAATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCT  
 CTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCGGATAAAACAGTCATTGAATATGA  
 ATATGATGTGAGAACCACTGACATTTGTGCGGGCCCTGAAGAGCAGGAGCTCAGTTTGCAGG  
 AGGAGGTGTCCACACAAGGAACATTATTTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCG  
 CAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA  
 CACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCTTGGTCGACTGGGATCCCC  
 AAACCTGGCAGGCTGTGTATTCCCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAG  
 CTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGCG  
 TCCAGACAGGCCACAGGAGAAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGT  
 TATATGTGCAGATGGAAAC**TGAT**GGCCAACACTTCCTTTTGCCTTTTGTTTCTGTGCAAC  
 AAGTGAGTCACCCCTTTGATCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTTCCAGT  
 TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTG  
 GTTCATGCATGTAGGTCTCTTAAACATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGT  
 GTTCTATGCAGAGAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGG  
 TGGGTGT

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## **FIGURE 62**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQRVFKELKLLTLCSSSQIGPPEVALTTDEKSISVVLTAPEKWKRNPECLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQ
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKEHPANLILYGNFED
KRFFVPAEKIVINFITLNISSDDSKISHQDMSLLGKSSDVSSSLNDPQPSGNLRPPQEEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDPKTVIEYEDVVRTDICAGPEEQELSL
QEEVSTQGTLLSQAAVLAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEESTTLVDWD
PQTGRCLCIPSLSSFDQDSEGECEPSEGDGLGEEGLLSRLYEAPADRPPEGNETYLMQFMEEW
GLYVQMEN
```

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 140-163

#### **N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

**FIGURE 63**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCC  
TCTGCC**AT**GGGGGCTCGGGTTGAGGGGCTGGGGACGTCCTCTGCTGACTGTGGCCACCGCCCT  
GATGCTGCCCGTGAAGCCCCCGCAGGCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGG  
TGACCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGA  
GGCTTCCTGCTGCGAGCCCGTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT  
CCGCACTGGCCTGGTGGTGTGGGCGCCACGTCTGAGTACTGCGGAGCCCAACCAGCAGG  
TGTTTGGCATCGATGCTCTACCACGCACCCGACTACCACCCCATGACCCACGCCAACGAC  
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCTGGGCCCTGCAGTGGGGCTGCTGAGGCT  
GCCAGGGAGAAGGGCCAGGCCCCCACAGCGGGGACACGCTGCCGGGTGGCTGGCTGGGGCT  
TCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGTGGAC  
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG  
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCTGGTGTGCAGGA  
ACCGGGCTCACGGCTCGTTTCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCGAC  
GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTGCGCGGAGCAGTCC  
CCAGCCCGGCCCTGCCTGGGACCACCAGGCCCCAGGAGAAGCCGCC**TGA**GCCACAACCT  
TGCGGCATGCAATGAGATGGCCGCTCCAGGCTGGAATGTTCCGTGGCTGGGCCCCACGGG  
AAGCCTGATGTTACGGGTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA  
AAGGGCAGAAGCAAACCCAGTAAAATGTTAACTGACAAAAAAAAAAAAAAAAAAGAAA

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## **FIGURE 64**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPTQQVFGIDALTTHPDYHPMTHANDIC
LLRLNGSAVLGPAVGLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLLTLMCLTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY
TQVSAFVAWIWDVVRSSSPQPGPLPGTTRPPGEAA
```

### **Signal peptide:**

amino acids 1-30



## FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGACGAAAGCTCCGCGCCGACTCCGGACGCCGTGACGCCTGA  
CGCCTGTCCCCGGCCCCGGCATGAGCCGCTACCTGCTGCCGCTGTCCGGCTGGGCACGGTAG  
CAGGCGCCGCGCTGCTGCTCAAGGACTATGTACCGGTGGGGCTTGCCCCAGCAAGGCCACC  
ATCCCTGGGAAGACGGTCATCGTGACGGGCGCAACACAGGCATCGGGAAGCAGACCGCCTT  
GGAAGTGGCCAGGAGAGGAGGCAACATCATCCTGGCCTGCCGAGACATGGAGAAGTGTGAGG  
CGCAGCAAAGGACATCCGCGGGGAGACCTCAATCACCATGTCAACGCCCGGCACCTGGAC  
TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGACGAAAGATCATTGAAGAGGAGGAGCGAGT  
GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCCACTGGACCACCAGGAGCGGT  
TCGAGATGCAGTTTGGCGTTAACACCTGGGTCACTTTCTCTTGACAAACTTGCTGCTGGAC  
AAGTGAAAGCCTCAGCCCCCTCGCGGATCATCAACCTCTCGTCCCTGGCCCATTGTTGCTGG  
GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCTACT  
GCCAGAGCAAGCTCGCATCGTCTCTTACCAAGGAGCTGAGCCGGCGGTGCAAGGCTCT  
GGTGTGACTGTCAACGCCCTGCACCCGGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG  
CATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA  
GCCCCGAGCTGGCCGCCAGCCAGCACATACCTGGCCGTGGCGGAGGAAGTGGCGGATGTT  
TCCGGAAGTACTTCGATGGACTCAAACAGAAGGCCCGGCCCGAGGCTGAGGATGAGGA  
GGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCCGCTGTGGGCTTAGAGGCTCCCTCTGTGA  
GGGAGCAGCCCCCTCCAGATAACCCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCTCCAG  
ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCTTGGCACTACCTGAGCCGGGAGACCCAG  
GACTGGCGGCGCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGAGTGGAAGTGGC  
CTGCAGGTGAGCACTGCCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG  
AGGGGCCATCTGATGCTTCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC  
TGTGCACCTTGACAGGCCACGTGAGGAGGCCAGCGGTGCTGTCCGGGAGGGTTCCAAGGTG  
TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGTCCCTGTGGGACCT  
TGTGTCATGCATGCTCCTCTCTGAGCCTTGGTTCTTACGAGTGAGATGCTCAGAATAACTG  
CTGTCTCCCATGATGGTGTGTGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGG  
GGTGTGTTGCTGAGGGCTTCTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAGGTGTATCCC  
GAGTTCAAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGTACAGGACCTGGGA  
TTGCTGGGACTCCACCTTCTATCAATTCTCATGGTAGTCCAACTGCAGACTCTCAAC  
TTGCTCATTT

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# **FIGURE 66**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35932, pI: 8.45, NX(S/T): 1
MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTIVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNNARHLDLASLKSIREFAAKIIIEEERVVDILINN
AGVMRCPHWTTEDGFEMQFGVNHLLGHFLLTNLLLDKLKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPFIWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAEAEDEEVARRLW
AESARLVGLEAPSVREQFLPR
```

## **Signal peptide:**

amino acids 1-17

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**FIGURE 67**

GAAGTTGCGGAGCGCTGGC**AT**GTGGTCTCTGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG  
 GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGAC  
 CAGCGTGGCGCGCGCCCTGGCGCCCGAGCGCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC  
 GCGGGAGAGGGCGGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGCAT  
 GAGGATTCACAAACCCCTGTGGCTAACCCCTGCTGTGCATTTACTCTCATCAACCGCTGCA  
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG  
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCCTTTGAGGACCTTGAGGGAGCAGCAAGG  
 GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTTGCTT  
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAACCGGCTCTTTCTCTCA  
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCCTATGACATGGGGGATATTACCATGCC  
 ATTCATGGCTGGAGGAGGCTGTCACTCTCTCCGAGGATCTTACGGAGAGTGGGAAGACAGA  
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCCTTGTCTATTTCGGGCGAGGAA  
 ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCAGATAATAAGAGG  
 ATGGCCAGGAATGTCTTGAATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTGGTAGC  
 TGAGGCTGTCACTCCAGAGGCCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC  
 TATGTACAGCCCTGGGTTCCAGGCCACTCTCTACCAGATCCCTAGCCTCTACTGTTCCCTAT  
 GAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTATCCACCTGGA  
 GCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAAATTAGAGAAC  
 TTGCAAGCCATGGCTACAGAGGTCAGTGGTGGCATCAGGGGAGAAGCAGTTTACAAGTGGAG  
 TACCGCATCAGCAAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCCCTCAA  
 CCACGCATTGCTGCGCTCACAGGCCCTTGATGTCCGGCCCTCCCTATGCAGAGTATCTGCAGG  
 TGGTGAAGTATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTCACCAAGC  
 AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC  
 GGTGGAAGCTGGAGGAGCCACAGCCTTCACTATGCCAACCTCAGCGTGCTGTGGTTAGGA  
 ATGCAGCACTGTTTTGTGGAACTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT  
 GCTGGCTGTCTGTCTGTGGTGGGAGATAAGTGGGTGGCCAACAGTGGATACATGAGTATGG  
 ACAGGAATTCCGCAGACCCTGCAGCTCCAGCCCTGAAGACT**TGA**AAGTGTGGCAGAGAGAAGC  
 TGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGTAGGAGAGGAGAA  
 AGCAGAGCAGCCTCCTGGAAGAAGGCTTGTCACTTTGTCTGTGCCTCGCAATCAGAGGC  
 AAGGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCGAGCCACGGAA  
 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGAGTGGAGGCCTGAGAGGGGAAGTTTCTGG  
 AGTTTCAGATACTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTTCGATCAGTGGGTCT  
 TTTTGGCACTTTGAACCTTGACACAGGGACCAAGAAGTGGCAATGAGGACACCTGAGGAGG  
 GGGCTAGCCTGACTCCCAAGACTTTAAGACTTTTCCCAACTGCCTCTGTGCTGCTGCAGCCAAAG  
 CAGGGAGTGTCCCCCTCCCAGAAGCATATCCAGATGAGTGGTACATTATATAAGGATTTTT  
 TTTAAGTTGAAAACAACCTCTCTTTCTTTTGTATGATGGTTTTTAAACAGTCATTAAAA  
 ATGTTTATAAATCAAAA

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## **FIGURE 68**

MGPGARLAALLAVLALGTGDPERAAAARGDTFSALTSVARALAPERLLGLLRRYLRGEEARL  
 RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHVSLEASENIRALKDGYEKVE  
 QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRVTSAITDLYSPKRLFSLTGDDCFQ  
 VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGWKTEDASLEDALDHLAFAYFRAGNVSCALS  
 LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPHLQTRDTYEGLCQTLGS  
 QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ  
 RSVVASGEKQLQVEYRISKSALWKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG  
 GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLLSSVEAGGATAFIYANLSVPVVRNAALFWW  
 NLHRSGEGSDTLHAGCFVLVGDKWVANKWIEHYGQEFRRPCSSSPED

**Signal peptide:**

amino acids 1-19

## FIGURE 69

GAGATAGGGAGTCTGGGTTTAAGTTCCTGCTCCATCTCAGGAGCCCTGCTCCCACCCCTAG  
GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC  
ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAG  
CGCCAGGATGCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC  
TGGCTCAAGTTTTCTACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGGCCCTGGTCCT  
GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCCTTGAAAGTGCCTTCC  
TGGCTCCAGCCATCATCCTCATCTCCTGGGCGTCTCATGTTTCATGGTCTCCTTCATTGGT  
GTGCTGGCGTCCCTCCGTGACAACTGTACCTTCTCCAAGCATTCATGTACATCCTTGGGAT  
CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG  
ACTTCTGAACGACAACATTGGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA  
AACATCATGGACTTTGTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG  
GAGCAAGAATCAGTACCACGACTGCAGTGCCCTTGACCCCTGGCCTGTGGGGTGCCCTACA  
CCTGCTGCATCAGGAACACGACAGAAAGTTGTCAACACCATGTGTGGCTACAAAATATCGAC  
AAGGAGCGTTTTAGTGTGCAGGATGTCATCTACGTGCGGGGCTGCACCAACGCGGTGATCAT  
CTGGTTCATGGACAATACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT  
TCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC  
TCTGTCACTGATGGGCTCCTGGGGCCCGGTGCCAAGCCAGCGTGGAGGCGGCAGGCACGGG  
ATGCTGCTTGTGCTACCCCAATTAGGGCCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC  
TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACACA  
CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCCTGTGTGTAGGTCCCACGGCCTCTGCCTC  
CCCAGGGAGCAGAGCCTGGGCCTCCCTAAGAGGCTTTCCCGAGGCAGCTCTGGAATCTGT  
GCCACCTGGGGCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA  
GAGCCTGAGGCTCTGCTCAGGGCCCATTTTCATCTCTGGCAGTGCCCTGGCGGTGGTATTCAA  
GGCAGTTTTGTAGCACCTGTAATTGGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGG  
GCATCTGGGGAAGGGCAAGGAGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTTGGC  
CTCTTCTCAGCCTCCAGGTGCCTTGAAGCCTCTTGCAAGGGCGGCTGCTTCTTGAAGCCTA  
GTTTTTTTTTACGTGATTTTTGTAAACATTCAATTTTTTTGTACAGATAACAGGAGTTTCTGAC  
TAATCAAAGCTGGTATTTCCCGCATGTCTTATTCTTGCCCTTCCCCAACAGGTTTGTAA  
TCAAACAATAAAACATGTTTTGTTTTGTTTTTAAAAA

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**FIGURE 70**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863  
><subunit 1 of 1, 294 aa, 1 stop .  
><MW: 33211, pI: 5.35, NX(S/T): 3  
MPRGDSEQVRYCARFSYLWLFSLIIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAP  
AIILILLGVVMFMVSFIGVLASLRDNL YLLQAFMYILGICLIMELIGGVVALTFRNQ TIDFL  
NDNIRRG IENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC  
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAV IIFMDNYTIMACILLGILLPQFLG  
VLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 22-42, 57-85, 93-116, 230-257

GAGGAGCGGGCCGAGGACTCCAGCGTGCCCAGGTCCTGGCATCCTGCACCTTGTGCCCCCTGACACCTGGGAAGATGGCCGCCCCGTGGACCTTACCCTTCTCTGTGGTTTGTCTGGCAGCCACCTGATCCAAGCCACCCTCAGTCCCACTGCAGTTCTCATCCTCGGCCCAAAGTCATCAAAGA  
AAAGCTGACACAGGAGCTGAAGGACCACACGCCACCAGCATCTCTGCAGCAGCTGCCGTGCTCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACCGTCTGAAGCACAATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA  
GCCCTGGCCAATGACCCAGGAGCTGTGAGTACCATGCCATCCCCCTGGACATGGTGGCTGGATTCAACACCGCCCTGGTCAAGCAGACTCGTGAGTCTCCACATGACAGCTAGGCCGCAAGCCACCATCGCATGGACACCAGTGAAGTGGCCCCACCCGCCGTGGTCTCAGTGACTGTGCCAACGCCATGGGAGCCTGCGCATCCAACCTGCTGTATAAGCTCTCCTTCTCGGTGAACGCCCTTAGCTAAGC  
AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTGATCGAGGCTTCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTCCCTCAGCATTTGACCGTCTGGAGTTTGACCTTCTGTATCCTGGCATCAAGGCTGACACCATTCACTCTACCTGGGGCCAAGTTGTTGGACTCACAGGGAAGGTGACCAAGTGGTTCAATTACCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCCTTACGCCCTCATCGTGAGTCA  
GTGACCTGGTGAAGAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTCAATGGTCCCTGTTGGACTCTGTGCTTCTCGTAGAGTGGCCATCGGTGTAAGTCAAGCATCGGGCTGATCAATGAAGAAGCTGCAGATAAGCTGGGATCTACCAGATCTGTAAGATCTTAACTCAGGACCATCTCCGAGTTT  
TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCTGTGCTGGAAGTGTTTCCCTCCCATGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTACACCAAAGGTGACCAACTTATACTCAACTGAATAACATCAGCTCTGATCGGATCCAGCTGATGA  
ACTCTGGGATTTGGCTGGTTCGAACCTGATGTTCTGAAAAACATATCACTGAGATCATCCACTCCATCTGTCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCAGTGTCTATTGGTG  
AAGGCCTTGGGATTCGAGGCAGCTGAGTCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGGCCTTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGAAGCTGGGTGGGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTGCCTGTGAAAAA

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## **FIGURE 72**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIEKLTQELKDHNATSILQQLPLLSAM
REKPAAGGIPVLGSLVNTVLKHHIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNLQCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL
GAKLLDSQGKVTWKFNNNSAASLTMTPTLDNIPFSLIVSQDVVKAABAVALSPPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL
RPLFTLGLIEASSEAQFYTKGQQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSGVPVSLVKALGFEEAESSLT KDALVLTFASLWKPPSPVQS
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457



**FIGURE 73**

GAGCGAACATGGCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATTGGTGGTGGCGCTG  
 CTCATCGTTTGGCAGCTTCCCTCAGCCTCTGCCCAAAGAAAGAGAGATGGTGTATCTGA  
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAAATGAATGGAGACA  
 AGTTCGGTCGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT  
 CTCCAACCTGCATAGACAGTGTGTCGTTTGAAGCAAGCTGATGAAGAATTCCAGATCCTGGC  
 AAACCTCCTGGCGATACTCCAGTGCATTACCAACAGGATATTTTTGGCATGGTGGATTTTG  
 ATGAAGGCTCTGATGTATTTTCAGATGCTAAACATGAATTAGCTCCAACCTTTCATCAACTTT  
 CCTGCAAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGC  
 TGAGCAGATTGCCCGGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC  
 CAAATTATGCTGGTCCCCTTATGTTGGGATTGCTTTTGGCTGTTATTGGTGGACTTGTGTAT  
 CTTTGAAGAAGTAATATGGAATTTCTCTTTAATAAACTGGATGGGCTTTTGCAGCTTTGTG  
 TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCC  
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCAGTTTGTAT  
 GCTGAAACACACATTGTTCTTCTGTTTAAATGGTGGAGTTACCTTAGGAATGGTGCCTTTATG  
 TGAAGCTGCTACCTCTGACATGGATATTGGAAGCGAAAGATAATGTGTGTGGCTGGTATTG  
 GACTTGTGTATTATTCTTCAGTTGGATGCTCTCTATTTTTAGATCTAAATATCATGGCTAC  
 CCATACAGCTTTCTGATGAGTTAAAGGTTCCAGAGATATATAGACACTGGAGTACTGGAA  
 ATTGAAAAACGAAAATCGTGTGTGTTTGAAGAAAGAATGCAACTTGTATATTTGTATTAC  
 CTCCTTTTTTCAAGTGATTTAAATAGTTAATCATTAAACCAAGAAGATGTGTAGTGCCTTA  
 ACAAGCAATCCTCTGTCAAATCTGAGGTATTTGAAAAATAATTACCTCTTAACCTTCTCTT  
 CCCAGTGAACCTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAAATTGAAAA  
 CTACTACTTTGTTTTAGTTAGAACAAAGCTCAAACACTACTTTAGTTAACTTGGTCACTCTGAT  
 TTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCTTGACCAGGTGTTCCACATATGCC  
 TGTTACAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT  
 ACTTTACGCATCTTTCCTTTTGTAGTAGAGAAATTATGTGTGTATGTGGTCTTCTGAAATG  
 GAACACCATTTCTCAGAGCACAGCTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT  
 GCATATTTCTTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA  
 TCCTAAATACAGGATTATAATTTCTGCTTGTAGTATGGTGTAACTACCTTGTATTAGAAA  
 GATTTAGATTTCATTCATCTCCTTAGTTTTCTTTAAGGTGACCATCTGTGATAAAAAATA  
 TAGCTTAGTGCTAAATCAGTGTAACCTTATACATGGCCATAAAATGTTTCTACAAATTAGAGT  
 TTGTCACTTATTCCATTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGCACTCCCTGG  
 CCAGGCGCAGTGACTTACGCCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC  
 GAGGTGAGGAGTTCAGACCATCCTGGCCAACTGGTGAACCCCGCTCTACTAAAAATAT  
 AAAAATTAGCTGGGTGGTGGTGGCAGGAGCTGTAATCCGAGCTACACAGGAGGCTGAGGCAC  
 GAGAATCACTTGAACCTCAGGAGATGGAGGTTTCAAGTGAGCCGAGATCAGGCCACTGCACTCC  
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

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## **FIGURE 74**

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLEWNTNKRVPVIRMNGDKFR  
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFAMVDFDEG  
SDVFQMLNMNSAPTFINFFAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY  
AGPLMLGLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN  
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV  
VLFFSWMLSIFRSKYHGYPSFLMS

### **Signal peptide:**

amino acids 1-29

### **Transmembrane domains:**

amino acids 183-205, 217-237, 217-287, 301-321

[illegible]

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**FIGURE 76**

&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885

&lt;subunit 1 of 1, 536 aa, 1 stop

&lt;MW: 61450, pI: 9.17, NX(S/T): 7

MLLLWVSVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSDFGRILTFHFGSQVVKLPFINF  
MKTRGTSFLNAYTNSPICCPSSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ  
KFGKLDYTSGGHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRTKVRVMERDWQNTDKAVNW  
LRKEAINYTEPFVIYLG LNLPHYPSPSSGENFGSSSTFHTSLYWLEKVSHDAIKIPKWSPLS  
EMHPVDYYSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVII  
SSDHGELAMEHRQFYKMSMYEASAHVPLMMGPGIKAGLQVSNVSLVDIYPTMLDIAGIPL  
PQNLSGYSLLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGAS  
ILPQLFDLSSDPDELNTNAVVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG  
QNYSNVIANLRWHQDWQKEPRKYENAIQWLKTHMNPRV

**Important features:****Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,  
498-501**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

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## FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG  
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**  
 GCCTCTCTTGGCCTCCAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT  
 GGTGGCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTGCGGTGCCAGCATTGTGACAG  
 CAGTTGGCTTCTCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATACCCAG  
 TGTGACATCTATAGCACCTTCTGGGCTGCCCGTGACATCCAGGCTGCCCAGGCCATGAT  
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA  
 CAGTCTTCTGCCAGGAATCCCAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC  
 ATCCTTGGAGGCCTCCTGGGATTCAATTCCTGTGCTGGAATCTTCATGGGATCCTACGGGA  
 CTTCTACTCACCACTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG  
 GCATTATTTCTCCCTGTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCC  
 CAGAGAAATCGCTCCAACCTACTACGATGCCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC  
 TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT  
 ATGTG**TGA**AAGAACCAGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG  
 CACCCCGAGGGCCACAGGTGAGGGACACTACCCTGGATCGTGTCAGAAGGTGCTGCTGAGG  
 ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG  
 CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC  
 CCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATCCCTTAAGCCAGGACTCAGAGG  
 ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCTAATCACATCCCACTG  
 ACTGACCTCTGTGATCAAAGACCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG  
 GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC  
 TCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCC  
 AGACTAATTTGTGCATGAAGTGAATAAAACCATCCTACGGTATCCAGGGAACAGAAGCAG  
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

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## **FIGURE 78**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVG IYLG LLLGLTLVAMLLPSWK TSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS
SQNRNSNYDAYQAQPLATRSSPRGQPPKVKSEFNYSYSLTGYV
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

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## **FIGURE 79**

GCAC TGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGC  
 TTATGTGTCAGTCTGTCTCCTCCTCTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG  
 AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGAGAGAG  
 TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC  
 CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTTG  
 TGAAGCTGAAGGTTCAAGGTGTGAATCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT  
 GAAAGCAGAAGACGTTTTCCCTGAGAAGACATAGAAAGAAAATCAACTTTCAC TAAGGCATC  
 TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTACAAAATG  
 ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT  
 AGATTATCAGGAAATAAATAAAGTGTTTTTCCAATGTACACACCTGTAAAA

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# **FIGURE 80**

MVPRIFAPAYVSVCLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYND AIVSLSE  
TRQCGPPCTFWPCFELCCLDSFGLTND FVVKLKVQGVNSQCHSSPISSKCESRRRFP

**Signal peptide:**

amino acids 1-25



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**FIGURE 81**

CTCCACTGCAACCACCCAGAGCC**ATGG**GCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT  
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT  
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCTGCAGCACTGTT  
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA  
GTCTGCTTTGAGCAGTGTCTGCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGA  
CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTCA**GCTAA**TGGAACATCAGGGGAA  
CGATGACTCCTGGATTCTCCTTCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTTACCTGAGA  
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCACTTCATT  
CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAG  
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCTCCTGAT  
GACCCCTATGGCCAACATCAACCCGGCACCACCCAAGGCTGGCTGGGGAAACCTTCACCCCT  
TCTGTGAGATTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA  
TAAATTTATGTACTTTATAAATGAAAA

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## **FIGURE 82**

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP  
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

**Signal peptide:**

amino acids 1-24

**FIGURE 83**

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCGCAGCGCTCACTCGCTCGCACTCAG  
 TCGCGGGAGGCTTCCCCGCGCCGGCCGCGTCCCGCCCGCTCCCCGGCACCAGAAAGTTCTCTCT  
 GCGCGTCCGACGGCGACATGGGCGCTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA  
 TCCCTGCTCTTCGCTCTCTTCTGGCTGCGTCCCTAGGTCGGGTGGCAGCCTTCAAGGTGCG  
 CACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGCGAAGCTCACCTCACCTGCAGGCTCT  
 TGGGCCCTGTGGACAAAGGGCAGCATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG  
 GCGAGGTGCAGACCTGCTCAGAGCGCCGCCCATCCGCAACCTCAGTTCCAGGACCTTCA  
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC  
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCTGCTG  
 GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACCTCGGAGCACAGGGT  
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAGCAAGATGCACCATCCAACCTGTGTGGTGT  
 ACCCATCTCTCTCCAGGATAGTGAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC  
 ATCGTAGGAATCCTCTGCTCCCCCTCATCTGCTCTGGTCTACAAGCAAAGGCAGGCAGC  
 CTCAAACCGCCGTGCCAGGAGCTGGTGGGATGGACGCAACATTCAAGGGATTGAACACC  
 CCGGCTTTGAAGCCTCACACCTGCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG  
 TCCTATGTGGCCAGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTCGGAGCCAGCAC  
 CCCCTGTCTCTCCAGGCCCGGAGACGTCTTCTCCCATCCCTGGACCCTGTCCCTGACT  
 CTCAAACCTTTGAGGTCACTTAGCCAGCTGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG  
 GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCTCCTTGGCTCGGCCCTGGTTC  
 CCTCCCTCTGCTCTGGGCTCAGATACTGTGACATCCAGAAGCCAGCCCCCTCAACCCCTC  
 TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTTTGGGGTGTGAG  
 ATTCTCCCTAGAGACCTGAAATTCACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA  
 GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA  
 GCATCAGTGGGACAAGATGGACATGGGCCACCTCCAGGCACCAGACACAGGGCAGCGTG  
 GAGAGACTTCTCCCCGTGGCCGCCCTTGGCTCCCCCGTTTGCCCGAGGCTGCTCTTCTGTG  
 AGACTTCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCCATGGCCATCGCC  
 ACCTTCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT  
 CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC  
 ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGCAATCTGAGGCCAGGACAG  
 ATGTTGCCCCACCCACTGGAGATGGTGCTGAGGGAGGTGGGTGGGGCCTTCTGGGAAGGTGA  
 GTGGAGAGGGGACCTGCCCCCGCCCTCCCCATCCCCTACTCCACTGCTCAGCGCGGGCC  
 ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT  
 GCTATTA AAAA CTACATGGGGAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

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## **FIGURE 84**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897

><subunit 1 of 1, 311 aa, 1 stop

><MW: 33908, pI: 6.87, NX(S/T): 6

MGVPTALEAGSWRWGSLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPDVK  
GHDVTFYKTWYRSSRGEVQTCSEERRPIRNLTQDLHLHHGGHQAANTSHDLAQRHGLESASD  
HHGNFSITMRNLTLDDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSSQ  
DSENITAAALATGACIVGILCLPLILLVYKQQAASNRRRAQELVRMDSNIQGIENPGFEAS  
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 190-216

## FIGURE 85

CCCACGCGTCCGCGCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT  
TTCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCCTGCCCTCC  
TTTCTGCCCCACGCTGCTTCTTGGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG  
GGTCTGTGGGTGATCTGTGGCCCTGTGCCTCCGTGTCTTTTCGTCTCCCTTCCTCCCGA  
CTCCGCTCCCGACCAGCGGCTGACCTGGGAAAGGATGTTCCCGAGGTGAGGGTCTC  
TCCTCCTTGCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCAGCTCGAGCCCGCCC  
AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCCGGCAGAGCTGGCACCCTACT  
TGGAGCCACAAGGCCTGATGTACTGCCTGCCTGTACCTGCTCAGAGGGCGCCCATGTGAGT  
TGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATG  
CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACAAAGTCTGCC  
AGCACAACGGGACCATGTACCAACCGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCTCC  
CGCTGCCCAACCAAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTCGGGCTCAC  
AACCTGCCCCGAACCAGGCTGCCCAGCACCCTCCCACTGCCAGACTCCTGCTGCCAAGCCT  
GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTG  
AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCACAGC  
CCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCAAGGGAGCAG  
GCAGCACAACCTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGG  
AAGACGTACTCCACGGGGAGGTGTGGCACC CGCCTTCCGTGCCTTCGGCCCTTGCCTG  
CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT  
ACCCCTGCCGTCACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTGCCCAGAGGACAAA  
GCAGACCTTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGTCTCT  
CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGG  
CCTCGGACTTGGTGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAACTGAGGCTCAG  
AGAGGTGAAGTACCTGGCCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA  
AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCAC  
GAAGGTCACTGGAACGTCTTCTAGCCCAGACCCTGGAGCTGAAGGTACGGCCAGTCCAGA  
CAAAGTGACCAAGACATAACAAAGACCTAACAGTGCAGATATGAGCTGTATAATTGTTGTT  
ATTATATATTAATAATAAGAAGTTGCATTACCTCAAAAAAAAAAAAAAAAAAAAAA

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# FIGURE 86

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHYPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPCPVTEPQQCCPKCCEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFPSRLPNQCVCSCCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDDED
SVQSLHGVVRHPQDPCSSDAGRKRGPPTAPFTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTTEYPCRHPKAVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLK
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSDPG
AEGHGQSRQSDQDITKT
```

**Signal peptide:**

amino acids 1-25



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**FIGURE 88**

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA  
TLQEAATTQENVAWRKNWMVGGEGGASGRSP

**Signal peptide:**

amino acids 1-18



[illegible]

**FIGURE 90**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLLLILFLLSWGPLQGQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKM  
LPILLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR  
RNEYDMVTDGTYISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL  
RDFTLAMAARKASRVVPFPWVG TGQLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLAN  
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCIAKLDPQTLDEQ  
QWDTPCPRENAEAAAFVICGTLVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH  
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV

**Important features:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 177-180, 248-251

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**FIGURE 91**

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG  
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCTCTTCTCTAATCCAT  
 CCGTCACCTCTCTGTCTATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**  
 CTCTCATGCTCAGTTTGGTTCTGAGTCTCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT  
 GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTCTCTGTTTCTCTGTC  
 TCCTAAGACCAATGCAGAGGCCATGGAAGTCCGTTCTTCAGGGGCCAGTTCTCTAGCGTGG  
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG  
 ACAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTAC  
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCACTTACTACCAGAAGGCCA  
 TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCTCTCATTTCATCACGGGATATGTT  
 GATAGAGACATCCAGCTACTCTGTCTCAGTCTCGGGCTGGTTCCCCGGGCCACAGCGAAGTG  
 GAAAGGTCCACAAGGACAGGATTTGTCCACAGACTCCAGGACAACAGACAGATGCATGCATGCC  
 TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCTGTTCATG  
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTTCGA  
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG  
 GCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCAGTGGAATAACAGGCGGAACCTGGAC  
 TGGAGAAGAAAGCACGGACAGGCAGAAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGAC  
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACGTAAACCCATA  
 GAAAAGCTCCCCAGGAGGTGCCCTACTCTGAGAAGAGATTACAAGGAAGAGTGTGGTGGCT  
 TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG  
 GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG  
 ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTCTCAATTAATCCCCGT  
 TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGTCTTCTCTGGACTATGAGTG  
 TGGGACCATCTCCTTCTCAACATAAAATGACCAGTCCCTTATTTATACCGTGACATGTCCGT  
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACCTCC  
 ATAGTCATCTGCCAGTCACCCAGGAATCAGAGAAAGAGGCCCTTTGGCAAAGGGCCTCTGC  
 AATCCCAGAGACAAGCAACAGTGAGTCTCTCTCACAGGCAACCACGCCCTTCTCCCCAGGG  
 GTGAAATG**TAG**GATGAATCACATCCACATTCTCTTTAGGGATATTAAGGTCTCTCTCCCA  
 GATCCAAAGTCCCGCAGCAGCCGGCCAAGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCC  
 ACATGGGAGTCAAGTGTCTATGGCTGCCCTGAGCTGGGAGGGGAAGAAGGCTGACATTACATT  
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAATACCACCTCTCAGGTGAAGAACCG  
 TCAGGAATTCACATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC  
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA  
 AAAAAA

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## **FIGURE 92**

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAAFSCFLSPKTNAEAMEVRFFRGQFSS  
 VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQK  
 AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFFRPTAKWKGPQGQDLSTDSTNRDMH  
 GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF  
 FGIVGLKIFFSKFQWKIQAELDWRKKGQAEIRDARKHAVEVTLDPETAHPKLCVSDLKTVT  
 HRKAPQEVPHSEKRFTRKSVVASQS FQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS  
 PDHGYWVLRNLNGEHLTYFTLNPRFISVFFRTPPTKIGVFLDYECGTISFFNINDQSLIYTLTC  
 RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASQWRASAIPESSSESSSQATTFFLP  
 RGEN

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255

**FIGURE 93**

GCGATGGTGCGCCCGGTGGCGGTGGCGGCGCGGTGCGGAGGCTTCCTTGGTCGGATTGCA  
 ACGAGGAGAAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC  
CATGAGGAGCCTGCCGAGCCTGGCGGCGCTCGCCCTGTTGTGCTGCGCCGCCGCCGCCGCCG  
 CCGTCGCCTCAGCGCCTCGCGGGGAATGTACCGGTGGCGCGCGGGCGCGGGGCGAGGTG  
 GACGCGTCGCCGGGCCCCGGGTGCGGGGCGAGCCAGCCACCCCTTCCCTAGGGCGACGGC  
 TCCCACGGCCAGGCCCGAGGACCGGGCGCCGCGCCACCGCTCCACCAGCCCTGGCTG  
 CGACTTCTCCAGCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCCTCTTCC  
 ACCACCTTTAGGCGCGCTCGGCCCTCGCGGACCACCCCTCCGGCGCGGAACGCACCTTC  
 GACCACCTCTCAGGCGCCGACCAGACCCGCGCCGACCACCTTTGACGACCACTGGCCCCG  
 CGCCAGCACCCCTGTAGCGACACCGTACCGGCGCCACGACTCCCGGACCCCGACCCCC  
 GATCTCCCCAGCAGCAGCAACAGCAGCGTCTCCCCACCCACCTGCGCCACGAGGCCCTC  
 TTCGCCTCCTCCAGAGTATGTATGTAAGTGTCTGTGGTTGGAAGCCTGAATGTGAATCGCT  
 GCAACCAGACCAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAACC  
 TGCAAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTAGCCATGTGACTGTAGTCC  
 ACATGGAGCTCTCAGCATACCGTGCAACAGGTAAGCAACAGAGGGTGAACTGAAGTTTATT  
 TTATTTTAGCAAGGGAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG  
 GAGGATGAGGGTCATAGATTTACAAAATATTTATATACTTTTATCTCTACTTTATATGT  
 TATATTTAATGTAGGATTTAAAAACATCTAATTTACTGATTTAGTCTCTCAAAGCACTAG  
 AGTCGCCAATTTTTCTCTGGGATAATTTCTGTAAATTTGATGGGAAAAAATTTATGAAGAAT  
 AAATCTGCTTTCTGAGAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAATGTTCTT  
 ATGTTTATTAATATACCATTTGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTTCTCTCTA  
 ATCAAAATTTCTACATTTGTTCTTTGGACATCTAAAGCTTAACCTGGGGTACCCTAATTTA  
 TTTAACTAGTGGTAAGTAGACTGGTTTACTCTATTTACCAGTACATTTTGAGACCAAAAG  
 TAGATTAAGCAGGAATATCTTTAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGA  
 ATAATGTACTGTTATCTAAGCATTTGCCTTGTACTGCACTGAAAGTAATTTATCTTTGACCT  
 TATGTGAGGCACCTTGGCTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAT  
 AATGAAAAAATAATGACAGGTTATACTCAGTGAACCTGGGTATAACCCAAGATCTGCTGC  
 CACTTACGAGCTGTGTCTTTGGGCAAGTAATTTCTTTCACTGAGCTGTTTTCTTCTCAAG  
 GTTGTGTGAAGATTAATGAGTTGATATATATAAATGCCTAGCACATGTCACTCAATAAA  
 TTCTGGTTTGTTTTAAATTTCAAAGGAATATATGGACTGAAATGAGAGAACATGTTTAAAG  
 ACTTTTAGCTCCTTGACAAAGAAGTGCTTTATACTTTAGCACTAAATATTTTAAATGCTTTA  
 TAAATGATATATCTGTTATGGAATATTGTATCATATTGTAGTTTATTAATAATGTAGAAG  
 AGGCTGGGCGCGGTGGCTCACGCCCTGTAATCCTAGCACTTTGGGAGGCCAAGGCGGGTGGAT  
 CACTTGAGGCCAGGAGTCTAGATGAGCCTGGCCAGCAGTGAAACCCGCTCTCTACTAAA  
 AATACAAACAAATTAGCTGGGCGTGGTGGCACACCTGTAGTCCCAGCTACTCGGGAGGCT  
 GAGGCAGGAGAAATCGGTTGAACCCGGGAGGTGGAGGTTGCGAGTGAGCTGAGATCGCGCACT  
 GCACCTCCAGCCTGGTGAGAGAGGGAGACTCTGCTTAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 94**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLPSLGLALLCCAAAAAASASAASAGNVTGGGAAGQVDASPGPGLRGEPSHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTLWATAGPSSTTFQAPLGPSPPTPPAAERTS
TTSQAPTRPAPTTLSTTTGPAPTTVPATTVPAPTTPTPTPDLPSSSNSSVLPTPPATEAPS
SPPEYVCNCSSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP
HGALSIPCNR
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

**EGF-like domain cysteine pattern signature.**

amino acids 214-226.

# FIGURE 95

TGCGGCGCAGTGTAGACCTGGGAGG**ATG**GGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG  
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGG  
CCCTGGTACGTGCTTGGGTGGCCTCCCGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA  
GAACGTCGTGGGGGTGGTGGTGACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC  
AGCACGGGTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAAACTCCGGATGG  
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA  
CTATGCCATCATCTTCACTCAGCTGGAGTTCCGGGACGAGCCCTTCAACACCGTGGAGCTGT  
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTACCAAGTGGAGCAGGAGC  
CTGGGCTTCCTGTACAG**TAG**CAGGCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAAGAT  
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCA  
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATT  
CACAGCA

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# **FIGURE 96**

MGGLLLAAFLALVSVPRQAQAVWLGRLDPEQLLGPWYVVLAVASREKGFAMEKDMKNVVGVVVT  
LTPENNLRTLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAIIIFTQL  
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

**Signal peptide:**

amino acids 1-20



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**FIGURE 97**

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCACAGACATGCTGCTGCTGCTGCTGCC  
 CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT  
 CCGTGACGGTGACAGGAAGGCCTGTGTGCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT  
 GGCTGGATTACCTTGCCCCAGTAGTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGA  
 CCAGGATGCTCCAGTGCCCAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC  
 GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCTGAGCATCAGAGATGCCAGA  
 AGAAGTGATCGGGGAGATACTTCTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA  
 ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG  
 GCACCTGGAGTCCGGCTGCCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG  
 GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC  
 CCGTCTCTCGGTGCTCACCCCTATCCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC  
 AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCCTCCATCTCAACGTGTCTTAC  
 CCGCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG  
 AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG  
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC  
 TCACAGCCCTCAAACCCGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA  
 ATTCACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC  
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTCGGGGGAGCTGGAGCCACAGCCCTG  
 GTCTTCTGTCTTCTGCGTCTATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG  
 GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAAACGCTGTGAGGGGTTAGCCT  
 CTCAGGGGCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAGCT  
 TCTGCCCCGTCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT  
 GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGCACCCGAGTACTCGGAGATCAAGATCC  
 ACAGATGAAGAACTGCAGAGACTCACCCCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGA  
 GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT  
 ATGAATTATGTGCAGAGTGAAGACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT  
 CCACACTGTGCCCTCCCTTTTATTTTTTTAACTAAAAGACAGACAAATTCCTA

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## **FIGURE 98**

MLLLLLPLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFYPSHGWIYPGPVVHGYWF  
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG  
SIKWNYPKHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVWPWACEQGTTPMISWIGTSVS  
PLDPSTTRSSVLTLPQPQDHGTSLTCQVTFPGASVTTNKTVHLNVSYPPQNLTMVTFQGDG  
TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV  
HLRDAAEFTCRAQNPLGSQQVYLNVSLSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS  
CRKKSARPAAGVGDGTIEDANAVRGSSASQGPLEPWAEDSPPDQPPPASARSSVGEGLQYA  
SLSFQMVKFPWDSRGQEATDTEYSEIKIHR

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

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**FIGURE 99**

GACGCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCTCTG  
GGTGTACAGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCCCTGGAGGAGGAGGATATCACAGG  
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCGGGAGGACAGGAGGCCAGGA  
AGGTGTCCCGAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC  
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA  
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGGAGGGACCACT  
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCTGCTCCACATGGGAAAGCTTGTGGGT  
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG  
ACTCTCGGAGGAGGACATTTTCACGCCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTTAGG  
CAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAGACACAGAGCCCGGACCACCT  
GGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCACCCACCTGACTCCAAATAAAGTCCT  
TTTCCCCCAA

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# **FIGURE 100**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVS PVKV TALGGGKL  
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH  
MGKLVGRNSDTNREAL EEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

**Important features:**

**Signal peptide:**

amino acids 1-17

# FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC  
 AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC**ATG**AGGATTCTGCAATTAA  
 TCCTGCTTGCTCTGGCAACAGGGCTTGTAAGGGGAGAGACCAGGATCATCAAGGGGTTCCAG  
 TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCGGCTACTCTGTGG  
 GCGCAGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA  
 TAGTTCACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC  
 ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA  
 CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC  
 TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCGGGCTGGGGCAGCACGTCC  
 AGCCCCAGTTACGCCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTGAGCACCA  
 GAAGTGTGAGAACGCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG  
 AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCAGTCTCTT  
 CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCATCACCCGAAAGCCTGGTGTCTACAC  
 GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT**TAG**ACTGGACCCA  
 CCCACCACAGCCCATCACCTCCATTTCCACTTGGTGTTTGGTTCCTGTTCACTCTGTTAAT  
 AAGAAACCCTAAGCCAAGACCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG  
 CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATCTGCCTT  
 GAAATATTGTGACTCTGGGAATGACAACACCTGGTTGTCTCTGTTATCCCCAGCCCCA  
 AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTGCTAAATGAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 102**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGTSCSLISGWGSTSSPQLRLPHTLRANITIIHQKCNAYPGNITDTM
VCASVQEGGKDCSQGDSGGPLVCNQSLQGIISWGDPCAITRKPGVYTKVKYVDWIQETMKN
```

### **Important features:**

#### **Signal peptide:**

amino acids 1-18

#### **Serine proteases, trypsin family, histidine active site.**

amino acids 58-63

#### **N-glycosylation sites.**

amino acids 99-102, 165-168, 181-184, 210-213

#### **Glycosaminoglycan attachment site.**

amino acids 145-148

#### **Kringle domain proteins.**

amino acids 197-209, 47-64

#### **Serine proteases, trypsin family, histidine protein**

amino acids 199-209, 47-63, 220-243

#### **Apple domain proteins**

amino acids 222-249, 189-222

# **FIGURE 103**

GAGCAGTGTCTGCTGGAGCCG**ATG**CCAAAAACCATGCATTCTTATTTCAGATTTCATTGTTT  
TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA  
GTGAAAATAGAAGTTTTGCATCGTCCAGAAAACCTGCTCTAAGACAAGCAAGAAGGGAGACCT  
ACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA  
CACAAAATGAAGGCCACCCCAATGGTTTGTCTTGGTGTGGGCAAGTCATAAAAGGCCTA  
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT  
TGCATACGGAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTTG  
AGATTGAACCTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC  
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA  
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAGATATTTTTAAGA  
AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT  
GAACTAT**TAG**CATATTTTGATTTCTACTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA  
AAACAAAGTCACCTTTTCTCCAAGTTGTATTTGCTATTTTCCCTATGAGAAGATATTTTGA  
TCTCCCAATACATTGATTTTGGGTATAATAAATGTGAGGCTGTTTGCAAACTTAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 104**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSTKSGDLLNAHYDG
YLAkdGSKFYCSRTQNEGHPKWFVLGVGVQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDDHGDGFI SPKEYNVYQHDEL
```

### **Important features:**

**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

**N-glycosylation site.**

amino acids 45-48

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 87-223, 129-142

**EF-hand calcium-binding domain proteins**

amino acids 202-214, 195-214



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# **FIGURE 105**

CAGAAATGCAGGGACCATTGCTTCTTCCAGGCCTCTGCTTTCTGCTGAGCCTCTTTGGAGCT  
GTGACTCAGAAAACCAAACTTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA  
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTACATTCC  
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCCAGTTCTTTGGGAAG  
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC  
CCCGTGTCTACTAAAAATACAAAAATCAGCCGGGCGTGGTGGTGCATGCCATCCCAGT  
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCAGGAGGCAGAAGTTGCAGTGAACCC  
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA  
TAGTTTCTTGTTTCATTTTCGCGACTGCCCTCTCAGTGTTCCTGGGATCCCCTCCCAAATAA  
AGTACTTATATTCTC

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## **FIGURE 106**

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHTCTCNHGYTSGSGQKLFTFPL  
ETCNARHGG SRL

**Signal peptide:**

amino acids 1-18

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# **FIGURE 107**

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGCAC  
 AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCAGACTTTGGAAGTGACCCACC**ATGG**  
 GGCTCAGCATCTTTTGTCTCCTGTGTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT  
 TTCAATGGCACTGAGTGTGGGCGTAACCTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC  
 CAGCCTGCGCTGCGGGGGTGTCTTATTGACCACAGGTGGGTCTCACAGCGGCTCACTGCA  
 GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG  
 CAGATCCGCGACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA  
 CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCGCGTAACGAGCAGCGTTCAAC  
 CCCTGCCCCTGCCAATGACTGTGCAACCGCTGGCACCAGTGCCACGTCTCAGGCTGGGGC  
 ATCACCAACCACCCACGGAACCCATTCCC GGATCTGCTCCAGTGCCCTCAACCTCTCCATCGT  
 CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG  
 GCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGGCCCCTGGTGTGTGGGGGA  
 GTCCTTCAAGGTCTGGTGTCTTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG  
 AGTCTACACCTATATTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAAC**CTGAC**  
 CTGTTTCTCCACCTCCACCCCCACCCCTTAACCTGGGTACCCCTCTGGCCCTCAGAGCACC  
 AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTGGCCTGGGAACCTTCTTGGAACCT  
 TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA  
 ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

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# **FIGURE 108**

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH  
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRLPVRVTSSV  
QPLPLPNDCATAGTECHVSGWGITNHPRNPFDDLQCLNLSIVSHATCHGVYPGRITSNMVC  
AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGI PGVYTYICKYVDWIRMIMRNN

**Signal peptide:**

amino acids 1-17

## FIGURE 109

GCGGCCACACGAGCTAGCCGGAGCCGGAGCCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC  
CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCCATGTCGCGGCGAGCTCAGCA  
ACAGGTTCCAAGGAGGGAAGCGTTTCGGCTTGCTCAAAGCCCGCAGGAGAGGAGGCTGGCC  
GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA  
GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC  
TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG  
AAGATGATCTCAGAGGTGACAGGAGGGGTGAGTACACTATATCTACCGAGACTTTGTGAA  
CATGATGCTGGGGAACGGTCGGCTGTCTCAAGTTAGTCATGATGTTGAAGGAAAAGCCA  
ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCTGA  
GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCATACCTCCCTCCCGATCTTGCTGCCCTT  
CTTGACACACTGTGATCTCTCTCTCTCATTTGTTTGGTCATTGAGGGTTTGGTTTGTGTTT  
TCATCAATGTCTTTGTAAAGCACAATATCTGCCTTAAAGGGGCTCTGGGTCGGGGAATCC  
TGAGCCTTGGGTCCCCCTCCTCTCTTCTTCCCTCCTTCCCGCTCCCTGTGCAGAGGGCTG  
ATATCAAACCAAACTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCTC  
CTCACTTGGAGGAACAGCACTCTCCATCCTTTCAGAAAGTCTCAAGCCAAGTTCAGGCTC  
ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG  
CTGCAGGGCCTCTTTCGGGTTTCCTTGGACAGTGCCATGGTTCAGTGCTCTGGTGTACCC  
AGGACACAGCCACTCGGGGCCCCGTGCCCCAGCTGATCCCACTCATTCACACCTCTTCT  
CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG  
TACCAGAAGGAACCTCCAGTCCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG  
CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTG  
GGGTTTGGGGGAAAGGTGAGCTCAGTGCTGTTCACCTTTTAGGGAGGATACTGAGGGGAC  
CAGGATGGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA  
CTGAGAAATACAAGGTGCTGTGCTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAA

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# **FIGURE 110**

MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAFFEKYMEFDLN  
NEGEIDLMSLKRMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVM  
MFEGKANESSPKPVGPPPERDIASLP

**FIGURE 111A**

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCA  
GGAGCGGGCCCTGACACACCATGGGCCCGGGTGGGCGAGGGTCGGCGCCGCGCTGCGCGCC  
CGCTGGCGCTGGCCTTGCGCTGGCGAGCGTCTTGAGTGGGCTCCAGCCGTGCGCTGCC  
CACCAAGTGTACTCTGCTCGCGCTGCCAGCTGGACTGCCAGGGCTGGGCTCCGCGCGGTTC  
CTCGGGGCTACCCCCGCAACGCTGAGCGCCTTGACTTGGACGAATAATATACCCAGGATC  
ACCAAGATGGACTTCGTGGGCTCAAGAACCCTCCGAGTCTTGCACTCTGGAGACAACAGGT  
CAGCGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA  
AGAATAAGCTGCAAGTCCTTCCAGAATTGCTTTTCCAGAGCAGCCGGAAGCTCACCAGACTA  
GATTTGAGTGAAAACAGATCCAGGGGATCCCGAGGAAGCGTTCCGCGGCATACCGATGT  
GAAGAACCCTGCAACTGGACAACAACACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC  
TGCGCGATTTGGAGATCCTTACCCTCAACAACAACATCAGTCGCATCCTGGTCACGAGC  
TTCAACCACATGCCGAAGATCCGAACCTCTGCGCCTCCACTCCAACCACCTCTACTGCGACTG  
CCACCTGGCCTGGCTCTCGGATTTGGCTGCGACAGCGACGGACAGTTGGCCAGTTCACTACT  
GCATGGCTCCTGTGCATTTGAGGGCTTCAACGTGGCGGATGTGCGAGAAGAAGGAGTACGTG  
TGCCACGGCCCCCATCGGAGCGCCCCATCCTGCAATGCCAACCTCATCTCCTGCCCTTCGCC  
TGCACGTGCGACAATAAATCCTGTGACTGTGAGGAAAGGGCTTGATGGAGATTCTCGCCA  
ACTTGCCGAGGGGCATCGTCGAAATACGCCTAGAACAGAACTCCATCAAAGCCATCCTTGCA  
GGAGCCTTACCCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA  
TATTGCTCCAGATGCCCTTCCAGGGCTGAAATCACTCAGTCGCTGGTCTGTATGGGAACA  
AGATCACCGAGATTGCCAAGGGACTGTTTGATGGGCTGGTGCCTTACAGCTGCTCCTCCTC  
AATGCCAACAGATCAAGTCTGCGGGTGAACGTTTACAGCTGCGAGACCTCAACTT  
GCTCTCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCGCCCCCTCTGCACT  
CCATCCAGACACTCCACTTAGCCCCAAAACCCATTTGTGTGCGCATGCCACTTGAAGTGGCTG  
GCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCCGCTGAGCAGCGCCGCGCG  
ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCGCTGCTCAGGCTCCGAGG  
ATTACCGCAGAGGTTACGACGCGAGTGCTTCATGGACCTCGTGGCCGAGAAGTCTCGC  
TGTGAGGGCAGGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCCAAGCCACTCCC  
TGAATATGTACCGACCTGCGACTGAAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA  
TCTTCAAGAAGTTGCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG  
CGAGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACCTGCT  
GGAGACCGTGACGCGGCGCGTGTTCGCTGGCCTCAGTGGCCTCAAACCTTGATGCTGAGGA  
GTAACCTTGATCAGCTGTGTGAGTAATGACACCTTTGCCGCGCTGAGTTCCGTTGAGACTGCTG  
TCCCTCTATGACAATCGGATCAACCACCTACCCCTGGGGCCTTCAACACGCTTGTCTCCCT  
GTCCACCATAAACCTCCTCTCCAAACCCCTTCAACTGCACTGCCACCTGGCCCTGGCTCGGA  
AGTGGTTGAGGAAGAGCGGGATCGTCAGTGGGAACCCCTAGGTGCCAGAAGCCATTTTCTCTC  
AAGGAGATTCCCATCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG  
TAGCTGCCAGCTGAGCCCGCGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGCGAT  
GCAGCAACAAGGGGCTCCGCGCCCTCCCCAGAGGCATGCCAAGGATGTGACCGAGCTGTAC  
CTGGAAGGAAAACCACTAACAGCCGCTGCCAGAGAGCTGTCCGCGCTCCGACACCTGACGCT  
TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC  
ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCGCTCCACGCTTCAAC  
GGGCTGCGGCTCCTCGAGGTGCTAACCTTCCATGGCAATGACTTTCCAGCGTTCTCGGAAGG  
CTCCTTCAACAGCTCAGATCTCTTTCCCATCTGGCGCTGGGAACCAACCCACTCAGCTGTG  
ACTGCACTCTCGGTGGCTGTGCGAGTGGGTGAAGGCGGGGTACAAGGAGCCTGGCATCGCC  
CGCTGCAGTAGCCCTGAGCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTT  
CCAGTGCAAAGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCTGCTCTCCAGCC  
CGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCGGTGTGCTCGCC

TACAGCTACAAAGGCGAAGGACTGCACCTGTGCCATCAACACCTGCATCCGAAACCCCTGTCA  
GCATGGAGGACCATGCCACCTGAGTGACAGCCCAAGGATGGGTTCAGCTGCTCTGCCCTCTG  
TGGGCTTTGAGGGCAGCGGTGTGAGATCAACCCAGTAGCTGTGAGGACAACGACTGCGAA  
AAGATGCCACCTCCGCTGGAGGGGATCAACAACCTACGTGTGTATCTGTCCGCTAACTACAC  
ACGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCTGAGCTGAACCTCTGTCAGCAT  
AGGCCAAGTGCATCCCCCTGGACAAGGATTACAGTTCGAGTGTGTCCCTGGCTACAGCGGG  
AAGCTCTGTGAGACAGCAATGATGACTGTGTGGCCCAAGTGGCCGACGGGGCCAGTG  
CTGGAGACAATAATGGCTACATGACTGACCTGCCCAAGGCTTCAGTGACACTTCTGTG  
AACACCCCCACCATGGTCTACTGACAGACAGCCATGCGACCACTAGCATGCGGACAAAC  
GGGGCCCACTGCATCGTGTGCTACAGGAGGCCACTGCGCTGCCACAGGGCTTCGCGCG  
CCCCAGCTGCGAGAAGCTATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTGGAAGTGG  
CCTCGGCCAAGTCCGACCCAGGCCAACATCTCCCTCGAGTGGCCACTCAAGAGGACAAC  
GGCATCCTTCTCTACAAGGAGACAATAGCCCTGGCATGAGCTGTACACAGGCGCACTG  
CGCGCTGGTATGACAGCGCTGAGTTCCCTTCCAACCAAGTGTACAGTGTGGAGACAGCTGA  
ATGATGGGCGAGTTTTCAGATGTGGAGCTGTGAGCTTAACACAGACCTGAACCTAGTAGTG  
GACAAGAAGGACTCCAAGAGGCTGGGGAACTCCAGAAGCAGCCAGCAGCATGGGCATCAACAG  
CCCCCTTCACTTGGAGGACTCCCCACTCCACCCGGGCTCTCCGCTTGGCCGACGGGACGG  
ACCGGCTCTAGGCGGCTTCCACGGATGCATCATGAGGTGCGCATCAACAACAGACTGCAG  
GACTTCAAGGGCTCCCAACACAGCTGCTTGGGGTGTCAACAGGCTGCAAGTCTCTGACCGGT  
TGTCAAGCAGCGGCTGTGCCGCTCGTGAGAAAGGACAGCTGGTGTGCGAGTGGCGCCAG  
GCTGGACCGGCCACTCTGCGACAGGAGGAGCCCGGGACCCCTGCCTGGCCACAGATGGCCAC  
CATGAAAAATGTGTGCCAATGGGACCTCATACATGTGCAAGTGTGCCAGGGCATGTGGAG  
GGACTTGTGTGACAACAAGAAATGACTTGCCAATGCTGTGACGCTTCAAGTGTCAACATG  
GGCAGTGCCACTCTCAGACAAGAGGGGAGCCCTACTGCTGTGCCAGCCGGCTTTAGCGGC  
GAGCACTGCCAACAAGAGAAATCCGTGCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA  
GAAAGGTTATGCATCATGTGCCACAGCCTCAAGGTCGCCATGTGAATGTCTGTGGGGCT  
GTGGGCCGAGCTGCTGCCAGCCACCCGACAGAACGCGCGGAAATAGCTTCTGAGTGCAGC  
GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGGGCTGCTCTCGCGTGTTC  
C**TAA**GGCCCTCGCCGCTGCTGCCACCTCTCGCACTCCAGCTTGATGGAGTTGGGACAGC  
ATGTGGGACCCCTGGTGGATTAGCATGAGGAAATGAAGCTGGAGAGAGGTGAAGAAGA  
AGCAATATTAAGTATATTGTAATAAACAATAAATAGAATCTAAAAAAA  
AAAAAA



amino acids 1-27

# **FIGURE 113**

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTCCTCCGCA  
 GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT  
 CCGGCAGGCTTTGAGG**ATGA**AGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG  
 GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAAATATTCTCGAGGGCTGGCCTG  
 GACAATTACTGGGGCTTCAGCCTTGGAACCTGGATCTGCATGGCATATTATGAGAGCGGCTA  
 CAACACCACAGCCCGACGGTCTTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA  
 ACAGCTTCGCGTGGTGCAGACGCGGAAGCTGAAGGAGAACAACCACTGCCATGTCGCCTGC  
 TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA  
 GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG  
 AGTGGA AAAAAGGCTGTGAGGTTTCC**TAA**ACTGGAACCTGGACCCAGGATGCTTTGCAGCAAC  
 GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTATCTTGTCCCGTTTCTCCCAATA  
 TTCCTTCTCAAACCTTGAGAGGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT  
 TTAAATGTC

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# **FIGURE 114**

MKAAGILTIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP  
TVLDDGSIDYGIFQINSFAWCRRGKLENNHCHVACSALITDDLTDIICARKIVKETQGMN  
YWQGWKKHCEGRDLSEWKKGCEVS

**Signal peptide:**

amino acids 1-19

**FIGURE 115**

CAGGCCATTTCATCCCACTGTCCTTGTGTTTCGGAGCCAGGCCACACCGTCCTCAGCAGTGT  
 CATGTGTTAAAAACGCCAAGCTGAATATATC**CATG**CCCCCTATTAATACTTGATACATGGCTCCC  
 CATTGGTTTTTGGAGAAAAAGTTCAAGCTTTTTACCTTGGTGTCTGCCTGTATCCCAAGTGTTC  
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCCAGATCTGCTTCTCAC  
 CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA  
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAA  
 ACATTCAAGTCCCTGTCTCACATAGACCCTGATGTCTCTATCCATCTCTAAATGTCACCAG  
 CTTTGACTCAGTTGTTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGTC  
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA  
 CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG  
 TTATGACGAGAGAGTCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAAATGGTCCAAC  
 AGTCCGACCTTGCCAGTATGTGACCTTCTTGAGGTCTTTCTCAGACAAACAGAAAAATCTCC  
 CTCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC  
 TCTGGAAGCCATGTACATGCAGTGCCAGTCATTGCTGTTAATTCGGGTGGACCCCTGGAGT  
 CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCACCTTCTCAGAAGCA  
 ATAGAAAAGTTCATCCGTGAACCTTCTTAAAGCCACCATGGGCCTGGCTGGAAGAGCCAG  
 AGTGAAGGAAAAATTTTCCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACCAAAC  
 TGCTGGTAT**TAA**TCAGATTGTTTTTAAGATCTCCATTAATGTCATTTTTATGGATTGTAGACC  
 CAGTTTTGAAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAATAAA  
 CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACACACCTCCCTGTCCACTTTTCAGAAA  
 AACCATGTCTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG  
 TCATTCCATGTTTCAGCAGAGTATTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA  
 TAAATTTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAAGTGTGTATCATTATCAA  
 AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCAGATTCCAAT  
 CCACCGAAGTGTTCACTGTCTGTGTAGGGAATTTTGTGTTGTCCTGTCTTGTGCTGGATC  
 CATAGCGAGAGTGTCTGTATTTTTTTTAAAGATAATTTGTATTTTGCACACTGAGATATAA  
 TAAAAGGTGTTTATCATAAAAAATAAAAAAAAAA

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# **FIGURE 116**

MPLLKLVHGSPLVFGEKFKLFTLVSAIPVFRLARRRKILFYCHFPDLLLLTKRDSFLKRLY  
RAPIDWIEEYTTGMADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD  
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGR LTSQDWERVHLIVAGGYDERVLENVE  
HYQELKKMVQQSDLGQYVTF LRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV  
IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF  
TEQLYRYVTKLLV

**Signal peptide:**

amino acids 1-15

# **FIGURE 117**

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCATGTGTGGACTTCGCGATCTT  
CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC  
AAGCTGCAGGAATTCCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT  
GTGAATAGTGGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCTGTGGT  
CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC  
ATATCAATCCCAATAAGACATCGGACCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT  
CAATCTGGTGGTGGCAGTGTGAGTGAAAACCATGAGGAAAAAATTGTATGAAAATGGTGT  
GACTGATTCTCTGAAGAGTAACCTTTGCCCTCCTCTAAAGCTTTCAGAAGAATTATTAGATA  
AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCCCTCAGCCAGCATATGCTTGGTTTTGCT  
ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTG  
CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAGGCTTCTAGATGGGTAC  
TTGATAAAAAACATGACTCGGAAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT  
TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACCTCAGTCAACATATTTTCATTGACTC  
CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG  
CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTAACCACTCTGAA  
GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAATGGTCTGTACTCC  
AGAGAAAATTGAGCAGCTCAGATATTGTGAGCATGTGCTTTGTGAACTGTTGCAACTGCCA  
AACTGACTCCAGTTTCTGCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTATATT  
CCTAGAGAGACCCTCGTCCCTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC  
ATCTCCACACAAGTTTGATCCAGATCGTTTGGTGTGATGAATTAGTAATGAAAACCTTTTCTCT  
CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGCATATATGGTGACCACA  
GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA  
AACAAAGTATGAACCTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT  
ATTAAAATTTTATACATTTAAATCATTGTTAAATTGATTGAGGAAAAACAACCATTTAAAAA  
AAATCTATGTTGAATCCTTTTATAAACCAAGTATCACTTTGTAATATAAACACCTATTGTAC  
TTAA

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# **FIGURE 118**

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH  
 ERYGPVVSFWFGRRLVVSGLGTVDLKQHINPNKTSDPFETMLKSLRLRYQSGGGSVSENHMRK  
 KLYENGVTDSLKSINFALLKLSEELLDKWLSPETQHVPLSQHMLGFAMKSVTQMVMGSTFE  
 DDQEVIRFQKNHGTWVSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS  
 QHIFIDSLVQGNLNDQQILED SMIFSLASCIITAKLCTWAICFLTSEEVQKKLYEEINQVF  
 GNGPVTPEKIEQLRYCQHVLCE TVRTAKLTPVSAQLQDIEGKIDRFIIIPRETLVLYALGVVL  
 QDPNTWPSPHKFD PDRFDELMKTFSSLGFSGTQCEPELRFAYMVTTVLLSVLVKRLHLLS  
 VEGQVIETKYELVTSSREEAWITVSKRY

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 271-290

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# **FIGURE 119**

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACCTCCAGCCTCAGA  
 GACCGCCGCCCTTGTCCTCGAGGGCCATGGGCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC  
 CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT  
 ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCAGCTGG  
 TGGCGGCGCTCTCTGTCACCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA  
 GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT  
 GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCACTACGTATTGGTACATTTTGTCT  
 TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTCGTCACCGTCTTTGGGCTGAAA  
 AAGAAACCCTTCGATTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG  
 CCGCTTCGTATTCTGGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCTCGGAAACTGCTTC  
 TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA  
 GTGCTTTGTAATAAAATATGTTTGTAGTAACATTAAGACTTATATACAGTTTtaggggaca  
 ATTA



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## **FIGURE 120**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG  
 LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVT  
 EMALFVTVFGLKKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

# FIGURE 121

TCCCGGACCCTGCCGCCCTGCCACTATGTTCCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC  
 CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA  
 GTGCCCCGGAACGAGTGAAGGCCCTGGCATCAGAGTGCGCCAGCACCTGAGCCTGCCCTT  
 ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCGCCTCGTGCCAGC  
 AGCAGGCCCCGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCAGCGTGGGCTAC  
 AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACCTCACGGGTGC  
 CCACTCAGGTCACCTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG  
 ATCGGGTGCCACACCCAGGCCATCCGGGCAGCCAGGGTCTACTGGCCTGCGGTGTGGCT  
 CAGGGAGCCCTGAGGTCCAACATATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC  
 TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCCTGAGGCC  
 CTGCTGATCCGCACCCCATTCCTCCCTCCCATGGCCAAAAACCCCACTGTCTCCTTCTCCA  
 ATAAAGATGTAGCTC

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# **FIGURE 122**

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT  
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP  
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL  
IQNWPHYRSP

**Signal peptide:**

amino acids 1-20

**FIGURE 123**

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACT  
 GACTCGCTGCTGCTTCGTGTTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG  
 ATGATGGTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC  
 CGGGTGCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCT  
 CCTAGGGCTGCTGGCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC  
 CGAACCACAGCCCCCACCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC  
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA  
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC  
 TCGTGCCCCCAGTAAAGCTGTAGAGTTCACCAGGAACAGCAGATCTTCATCGAAGCCAAG  
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCCGACCTC  
 GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT  
 GGAGCTGCTCCCGAGCCCTTCAAAGTCGTCGTGTCTACATCGCCTTCTACAGCAGCGACTAT  
 CGGCTGGTCCAGAAGGTGTGCCCAGATTACAACTACCATAGTGATACCCCTACTACCCATC  
 TGGGTGAACCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCCTGCCCATGC  
 AGGAGACCATCTGGACACCGGGCAGGGAAGGGTTGGGCCTCAGGCAGGAGGGGGTGGAG  
 ACGAGGAGATGCCAAGTGGGGCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGTCCCAAGTG  
 CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT  
 CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC  
 TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT  
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTG  
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC  
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCTGAGCCCCTTGTCGTGTGCTGAGCATG  
 GCATGAGGTGAAGTGGCAACCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC  
 CAGCCAGGCCACCCCTTTCCAAAATTCCTCTCTTGCCAGTACTCCCCCTGTACCACCAATT  
 GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCTCCACACTAAGGCC  
 ACAGCCCATCCGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG  
 CATCCATGTCCCGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTGACAGCCGGGTTCTCC  
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGCACGGGTGGGGCGGGGCCGGCCGAGA  
 GCATGTGCTGGATCTGTTCTGTGTGCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGT  
 GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGGAGCAGGAATAAAGCTT  
 GCCCCGGGGCA

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## **FIGURE 124**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521

><subunit 1 of 1, 252 aa, 1 stop

><MW: 28127, pI: 8.91, NX(S/T): 5

MQLTRCCFVFLVQGSYLIVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN  
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD  
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR  
RTSLCTHDPKICSRDHAQSSATWSCSQFFKVVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPY  
YPSG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

**FIGURE 125**

GTGAATGTGAGGGTTTGATGACTTTCAGATGTCTAGGAACAGAGTGGGTGCAGGGGCCCA  
 GGCAGGGCTGATTCTTGGGCGGAGGAGTAGGGTAAAGGGTTCTGCATGAGCTCCTTAAAG  
 GACAAAGSTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT  
 TGGTGGAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGCAGCGCTGTGACCTAGCCGCTAG  
 CATCTTCCCGAGCACCCGGGATCCCGGGTAGGAGGCGACGCGGGCGAGCACCAGCGCCAGCC  
 GGCTGCGGCTGCCACACGGCTCACATGGGGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG  
 GCCGTGCTGCTGGTCTCACGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC  
 CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG  
 GCTCCTCTTCTCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTGCGCTTCTCG  
 GCGGTGCGGAGCACCAACCAGGACCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT  
 CGATCAGATCCTGGTGAATGTGGTAATTTTTCACATTGGAGTCTGTCTTTGTAGCACCAA  
 GAAAAGGAATTTACAGTTTCAGTTTTTTCACGTGATTAAAGTCTACCAGAGCCAACTATCCAG  
 GTTAACTTGATGTTAAATGGAAAACCAGTAATATCTGCCTTTGCGGGGGACAAAGATGTTAC  
 TCGTGAAGCTGCCACGAATGGTGTCTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA  
 AACTGGAGAAAGTAATTTGGTGGAGGCTGGCAGTATTCACGTTTTTCTGGCTTTCTGGTG  
 TTCCCCCTATAGGATTCAATTTCTCCATGATGTTTCATCCAGGTGAGGGATGACCCACTCCTG  
 AGTTATTGGAAGATCATTTTTTTCATCATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG  
 GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG  
 TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA  
 ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTCAATTTCTGGGATTACTGAATTAGT  
 TACAGATGTGGAATTTTATTGTTTAGTTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA  
 AAACCTTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAGAAGCTGTACTG  
 TGTTAATATATTGATTATATTGTTTTTATTCCTTTGGAATTAGTTGTTTGGTTCCTGTGTA  
 AAAACTTGGATTTTTTTTTTTCAGTAACTGGTATTATGTTTTCTTAAATAAAGTAATGAA  
 TGGCTTGCCACAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAAAA  
 GAATGCTTCATAGTTGATTTTTAATTGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT  
 TTCTAAGAAGAAGATAGATCAATAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG  
 TGTCTAATCCCTGAGCCTCAGCAAAACAGCTCCCTCCGAGGGAATCTTATACTTTATTGCT  
 TCAACTTTAATTAATAATGATTGATAATAACCACTTTATTAAAAACCTAAGGTTTTTTTTTT  
 TCCGTAGACATGACCACTTTATTAAGTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT  
 TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCCTTAACTCTTTAAATTGTA  
 TATATTTATCTGTTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTTAGTGCAATAT  
 CTTGTCTTTGTATAGGTCATATGAATTCATAAAATTTATTTATGTCTGTTATAGAATAAAGA  
 TTAATATATGTTAAAAAAA

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# **FIGURE 126**

MGSGRRALSAVPAVLLVLTLPGLPVWAQNDEPIVLEGGKCLVVCDSNPATDSKGSSSSPLGI  
SVRAANSKVAFSAVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTLESVVFVAPRKGIIYSFSF  
HVIKQVYSQTIQVNLMLNGKPVISAFAGDKDVTREAAATNGVLLYLDKEDKVYLKLEKGNLVG  
GWQYSTFSGFLVFPL

**Signal peptide:**

amino acids 1-27

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## **FIGURE 127**

CGGTGGCC**ATG**ACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC  
GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGAGC  
TTTCTTCTGGTTGGTGTCTCTACTGATTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTA  
TTGACAACAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC  
TATATCCAAGAAATGTTCCGATTGTCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT  
GAAGAGTATAAACCCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCT  
TGGGCTTTTGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCCTATCTGACTCCTTGGGG  
CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGAC  
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTGATGGCTGTGAGAAGA  
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC  
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGTGCTATGGGCAC  
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG  
ACAAGAAGTTTCTTCTTTACAACCAGCGCTCCAGAT**TAA**CTCAGGGGAACAGCACTTCCCAA  
ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTTTCTGAAAATCCCTTTTTCTG  
GTGGAATTGAGAAAGAAATAAACTATGCAGATA



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## **FIGURE 128**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDSLGP GTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFFDGCEKKKW
GILLIVLLTHLLVSAQTFISSYGINLASAFIILVLMGTWAF LAAGGSCRSCLKLLCQDKN
FLLYNQSR
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

#### **Glycosaminoglycan attachment site.**

amino acids 120-123

#### **Sodium:neurotransmitter symporter family protein**

amino acids 31-65

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# FIGURE 129

CGGCAACCAGCCGCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGC**ATG**TTGCTCTGGGCTTGCCCTTCT  
 TGGTGCTCTTGGTGGGCTCGGTGAGAGCCATCTGGGGGTCTTGGGGCCCAAGAACGCTCTCGCAGAAAGACGCCG  
 AGTTTGGAGCCACCTACGTGGACGAGGTCAACACGCGAGCTGGTCAACATCTACACCTTCAACCATACTGTGACCC  
 GCACAGGACAGAGGGCGTGGCTGTCTGTGAACGCTCTGAACAGCAGAGGGGGCGCGCTGTCTGTTTGTGG  
 TCCGCGAAGAGAGGGCTGTGGTGTCTTCCAGGTGCCCTAATCTGCGAGGGATTTTTCAGCGCAAGTACCTCT  
 ACCAAAGATGGACGAACTCTGTTCAGCCCCCACCAGAAATGAGTCGGAGATTCAGTTCTTCTACGTGGGATG  
 TGTCCACCTGTACAGGTCAACACCATACAGCTCCGGGTCAAGCGATGGACGATTTTGTGCTCAGGACTG  
 GGGAGCAGTTTCACTTCAATACCACAGCAGCAGCCCCAGTACTTCAAGTATGAGTTCCCTGAAGGCGTGGACT  
 CGGTAATTTCAAGGTGACCTCCAACAGGCCCTTCCCTGTCTCAGTCATCTCCATTACAGGATGTGCTGTCTCTG  
 TCTATGACCTGGACAAACAGTATGCTTTCATCGGCTGTACAGACGATGACCAAGAAAGGCGGCCATCACCGTAC  
 AGCGCAAGACTTCCCGAGCAACAGCTTTTATGTGGTGGTGGTGAAGACCGAAGACCAAGCCCTCGGGGGCT  
 CCTGCTCTTCTACCCCTTCGCAAGATGAACGGTTCGATCAAGGGCACCGCCAGAAACCTGTCAAGTGTGG  
 TGTCTCAAGCAGTCACTCTGAGGCATACGTCAAGTGGGATGCTCTTTGCTGGGTATATTTCTCTCCTTTTACC  
 TGCTGACCGTCTCTGCTGCTGCTGGGAGAACTGGAGGCAGAAAGAAAGACCTGCTGGTGGCCATTGACCGAG  
 CCTGCCAGAAAGCGGTCAACCTCGAGTCTGGCTGATTTCTTCTGGCAGTTCCCTTATGAGGGTTACAAC  
 ATGGCTCTTTGAGAAATGTTTCTGGATCTACCGATGGTCTGGTTGACAGCGCTGGCAGCTGGGACCTCTCTTACG  
 GTTACAGGGGCGCTCCTTTGAACCTGTAGGTACTCGGCCGAGTGGACTCCATGAGCTCTGTGAGGAGGATG  
 ACTACGACGATGACCGCATCGATTCCGACAAGAAATGTCACTTCGCAACCAAGCAATACCTCTATGTGGCTGACC  
 TGGCAGCGAAGGACAGCGGTGTCTGCGGAAAAAGTACCAGATCTACTTTGTGAAGATTTGCCAACTTGTCTGTCT  
 TCTATGCCCTTCTGTGGTGACGCTGGTATCACTACCAGACGGTGGTGAATGTACAGGGAATCAGGACATCT  
 GCTACTACAACCTTCTCTCGGCCCCCACTGGCAATCTGAGCGCTTCAACAACTCTCAGCAACCTCGGGGT  
 ACATCTCTGCTGGGCTGCTTTCTGCTCATCATCTCTGCAACGGGAGATCAACCAACACCGGGGCTGTCTGTGGA  
 ATGACCTCTGCTGGATGCTGGGATCCCCAAACACTTTGGGCTTTTCTACGCCATGGGCACAGCCCTGAGTA  
 TGAGGGGGCTGCTCAGTGTCTGCTATCATGTGTGCCCAACTATACCAATTTCCAGTTTGACATCATGTTCAATG  
 ACATGATCGCGGACTCTGATCTGAAGCTCTACAGAAAGCGGCACCGGACATCAACGCCAGCGCTCAGATG  
 CCTACGCTGCTGCTGGCCATTGTCTCTCTCTGCTGGGCGTGGTCTTTGGCAAAGGGAACCGGGCTGTCT  
 GGATCGTCTTCTCATCATTCATCACATCGCCACCCGTGCTCTCAGCAGCGACTCATTTAGATGGGCGCGTGGGA  
 AACTGGACTCGGGGATCTTCCGCCCATCTTCCACGTGCTCTACACAGACTGCATCCGGCAGTGCAGCGGGCGCG  
 TCTACGTGGACCGCATGGTGTCTGTTGATGGGCAACGTCACTCAACTGCTGCTGCTGGCTGCCATTGGGCTTATCA  
 TCGCCCCCAATGATTTGCTCTCTACTTGTGGCCATGGCATCTGCAACCTGCTCTGCTTTACTTTCGCTTCTACA  
 TCTATCATGAAGCTCCGGAGTGGGGAGGAGATCAAGCTCATCCCCCTGCTGCTCATGTTTGCACCTCCGTTGGTCT  
 GGGGCTTCGCGCTCTTCTTCTTCTTCCAGGGACTCAGCACCTGGCAGAAACCCCTGCAAGAGTCGAGGGAGTCA  
 ACCGGGACTGCATCTCTCGACTTCTTTGACGACCAAGACATCTGGCACTTCTCTCTCCATCGCATGTTTTCG  
 GGTCTTCTGGTGTGCTGACACTGGAAGACGACCTGGATACTGTGACGCGGACAAGATCATGTCTCT**TAGC**  
 AGGAGTGGGCTTGCCTTCACTCAAGGGCCCTGAGCTCCTTTGTGTATAGACGGCTCACTCTGTCTGCTGCT  
 GTGGGCTAGTCCAGCACCCGCTGCCAGCAGTGGATGGCAGAGGACAGCCAGGTCTAGCTTAGGCTTGGCTCT  
 GGGACAGCCTGCGGGTGGCATGGAACCTTGCAGCTGCCCTCTGCCAGGAGGCGCTGCTCCCTGGAACCCCC  
 AGATGTTGGCCAAATGCTGCTTTCTCTCAGTGTGGGGCTTCCATGGGCGCTGTCCTTTGGCTCTCCATTT  
 TGCTCTTTCAAGAGGAAGGATGGAAGGGACACCTCCCATTTTCATGCTTGCATTTTGGCGTCTCTCTCCCC  
 ACAATGCCCGAGCTGGGACCTTAAGCGCTCTTTTCTCCCATCACTCCCATCCAGGCGCTAGTCTGGGGCTGA  
 ATCTGTCTGTATACAGGCGCCAGTCTCTTTGGGCTGCTCCTGGCTGCCATCACTGCCATTCGCTCAGCTCAGCC  
 AGGATGGATGGGGGTATGAGATTTTGGGGGTGGCCAGCTGGTGCCAGACTTTTGGTGCTAAGGCTCGCAAGGGG  
 CTGGGGGAGTGGGATTTCTTCTTCTCCTCTGACCTGTGCTCAGGCTGGCTTTTAGCAATGCGCTCAAGCCAAAT  
 TGAAACCGCCTCTGATTCAAGAGGCTGAATTACAGAGGTCACCTCTTCACTCCCATCAGCTCCAGACTGATGCC  
 AGCAGCAGGACTGGAGGGAGCGGCTCACCCCTTCCCTTCTTCCAGGCGCTTAGCTTGTGCCAAACCCC  
 AGCTGTTGGGCTTTCAAGTGCATTTGACACTGCCCAAGAAATGCCAGGGGCAAGAGGGATGATACAGAGTTGAC  
 CGCGTTGCTGCTCCACAGCTGTGGGCAACCCAGTGCTACCTTAGAAAGGGGCTCAGGAAGGATGTGCTGTGTT  
 CCCTCTAGCTGCGCAGCTAGCTGCTCTAGGACCCAGGGCTGGCTCTAAGTTTCCGCTCAGCTCTCAGGCA  
 AGTTTCTGTTAGTCACTACACACATACCTATGAACCTTGGAGTTTACAAGAAATGCCCGAGCTCTGGGCAC  
 CTTGGCCACCTCTGCTTCTGGATCCCTTCTGTCACCCAGTGTGTCAGGATGGGAGGCGTCAAG  
 CGGGGCTGCTGTTTGGGATGGGAATGTTTTCTCCAAACTTGTGTTTATAGCTTCTGTTGAGGCTGGG  
 AGATGAGTGGGTCTGGATCTTTCTCAGAGGCTTCCATGCTATGTTGCATTTCCGTTTTCTATGAATGAATT  
 TGCATTCAATAAACACAGACTCAAAAAAAAAAAAAA

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## FIGURE 130

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHGLVLPKNVSKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLFLVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTEGQFSFNTTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFFPCSVISIQDVLCPVYDLNNAVAFIGMYQTMTKKAAITVQRKDFPSNSFYVVVV
VKTEDQACGGSLPFYPFAEDEPVDQGHRQKTLISVLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLVAIDRACPESGHPRVLADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDLISYGYQGRSFEPVGTFRPRVDSMSSVEEDDYDTLTDIDS DKNVIRTKQYLYVADL
ARKDKRVLRKKYQIYFWNIAITIAVFYALPVVQLVITYQT VVNVTGNQDICYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIILQREINHNRALLRNDLCALECGIPKHFGLFYAMGTALM
MEGLLSACYHVCNPTNFQFDTSMFYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNTAFWIVFSIIHIIATLLSTQLYMGWRKLD SGIFRRILHVLYTDCIRQCSG
PLYVDRMVLVLMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFQGLSTWQKTPAESREHNRDCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDDDLDTVQRDKIYVF
```

### Important features of the protein:

#### Signal peptide:

amino acids 1-18

#### Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

#### Leucine zipper pattern:

amino acids 497-518

#### N-glycosylation sites:

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

**FIGURE 131**

GCTCAAGTGGCCCTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC  
 TCTCTTCTTGGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTTGGGCGCTGGAGGGCCTGTCTGT  
 ACCATGGTCCCTGCTTGGCTGTGGCTGTCTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGC  
 CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAATTTCCCTTTATACC  
 TGACCAAGTTGGCCCTGCCCGTGGAGGGGCTGAAGGCCAGATCGTGTGTGAGGGGATCA  
 GGCAAGGCCAATGAGGGCCATTGTGCTATGGATCCAGATTCTGGCTTCCGTGTGTGAGCAGC  
 GGCCCTGGACCCAGAGGAGCAGGCAGAGTACAGCTACAGGTACCCCTGGAGATGCAGGATG  
 GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAAGGTG  
 CCCCATTCTCTCAAGGCATCTACAGAGCTCGGCTGAGCCGGGTACCAAGCCTGGCATCCC  
 CTTCTCTTCTTGTGAGGCTTACAGACCGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT  
 TCCACATCCTGAGCCAGGCTCCAGCCAGCCTTCCCCAGACATGTTCAGCTGGAGCCTCGG  
 CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC  
 CTACCAAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGGCCACCAAGGCCACTG  
 CCACCGTGGAAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA  
 GAGAATCTCAAAGTCCCTATACCCGACCCACATGGCCAGGTACACTGGAGTGGGGGTGATGT  
 GCATATCACCTGGAGGCCATCCCCCGGGACCCCTTGAAGTGAATGCAGAGGGAAACCTCT  
 ACGTGACCAGAGAGCTGGACAGAGAAGCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG  
 AATTCCCATGGCGAGGACTATGGGGCCCTCTGGAGCTGCACGTGCTGGTGTGGATGAGAA  
 TGACAACGTGGCTTATCTGCCCTCCCCGTGACCCACAGCTCAGCATCCCTGAGCTAGTCCAC  
 CAGTACTCAAGTGACTAGACTGTGACAGAGGATGCAGATGCCCCGGCTCCCCAATTTCC  
 CACGTTGTGTATGACTGCTGAGCCCTGAGCCTGAGGATGGGTGAGGGGAGAGCCTTCCA  
 GGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGTGTCTCCACTCCGAGCAGCCGGAACAA  
 TCCTGTCTTCTGGTGTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCAGCTGT  
 GAAGTCGAAGTCGCAGTCCACAGATATCAATGATCACGCCCTGAGGTTTACACTTCCAGAT  
 TGGGCCATATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCA  
 TTGATGCTGACCTCGAGCCCGCCTTCCGCCCTCATGGATTTGGCATTGAGAGGGGAGACACA  
 GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTTGCA  
 GAACCTCAGTTATGAGGCAGCTCCAAGTCTATGAGGTGGTGGTGGTGCAGAGTGTGGCGA  
 AGCTGGTGGGGCCAGGGCCAGGCCCTGGAGCCACCGCCAGGGTACTGTGCTAGTGGAGAGA  
 GTGATGCCACCCCCAAGTTGGACCAAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGGCCCC  
 AGCCGGCTCTTTCTGTGCTGACCATCCAGCCCTCCGACCCATCAGCCGAACCCCTAGGTTCT  
 CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTTCCGGGGAGGTGCACACC  
 GCCCAGTCCCTGAGGGGCGCCAGCCTGGGGACACCTACACGGTGTCTGTGGAGGGCCAGGA  
 TACAGCCCTGACTCTTGCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCAAGACCATG  
 GCTGTGATCGTGAGTGGACCCAGCAAGGACCCCGATCTGGCCAGTGGGCACGGTCCCTACAG  
 TTTACCCCTTGGTCCCAACCCCAAGGTGCAACGGGATTGGCGCCTCCAGACTCTCAATGGTTCT  
 CCAATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCAGTGAACACATAATCCCCGTGG  
 TGGTCAGCCACAATGCCAGATGTGGCAGCTCCGTTGAGTGTGATCGTGTGTGCTGCTGCAAC  
 GTGGAGGGGCGAGTCATGGCAAGGTGGGCCGATGAAGGGCATGGCCACGAAGCTGTCCGC  
 AGTGGGCATCCTGTAGGCACCTGTGTAGCAATAGGAATCTTCTCATCTCTATTTTCACCC  
 ACTGGACCATGCTCAAGGAAGAGGACCCGGATCAACAGCAGACAGCGTGCCCCGTGAAGGCG  
 ACTGTCTGCAATGGCCAGGAGCTTATGCTGGGAGCTTGGCCCTTGTGCTTGTGCTGAGTCCC  
 CTGGGAGAGAGCCAGCACCCAAAGATCCAGCAGGGGACAGGACAGTAGAAGCCCTCCATCT  
 CTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAAGCCCTGGACACCAAC  
 TTTATGGACTGCCCATGGGAGTGTCTCCAAATGTCAAGGTGTTTGGCCCAATAATAAGCCCCA  
 GAGAAGTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 132**

MVPAWLWLLCVSVQPALPKAQPaelSVeVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG  
KATEGPFAMDPDSGFLLVTRALDREEQAeyQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP  
HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRL  
GALALSPKGSTSLDHALERTYQLLVQVKMDGQASGHQATATVEVSIIESTWVSLEPIHLAE  
NLKVLPHHMAQVHWSSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAeyLLQVRAQN  
SHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPGTEVTRLsAEDADAPGSPNSH  
VVYQLLSPEPEDGVEGRAfQVDPTSGSVTLGLVPLRAGQNILLVLAMDLAGAEGGFSSTCE  
VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTaIDADLEPAFRlMDFAIERGDTE  
GTFGLDWEpDSGHVRLRLCKNLSYEAAPsHEVvvvvQSVAKLVGPGPGGATATVTVLVERV  
MPPPKLDQESYEASVPISAPAGSfLLTIQPSDPISRTLRFSLVNDSEGWLCIEKfSGEVHTA  
QSLQGAQPGDTYTVLVEAQDTALTlAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF  
TLGPNPTVQRDWRLQTlNGSHAYLTlALHWVEPREHIIPVVVSHNAQMWQLLVRIIVCRcNV  
EGQCMRKVGRMKGMPTKLSAVGILVGTLVAIGIFLILIFTHWTMSRKKDPDQADSVPLKATV

### **Signal peptide:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 762-784

**FIGURE 133**

CCGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA  
 GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATACGCAA  
 ATTGAGTCAACTAGTGAAATCAAACAACCTGAAGCTCAATTTCTGGAATCTCCCTCTCTCT  
 TCAATCGGCTGTGGATGCTTGGTCCCATCTGTCACTGTGAGCAGCATTTAAATCCTTCTCTG  
 AGATCCCAGGGCTTAGAGTACCGAGTGACAAATGAGGACCTGCAGGCCCTTTTAGACAATGA  
 AGATGATGAAATGCAACACAATGAAGGGCAAGACGGAGCAGTAATACTCAACTACGGGG  
 CTTACCATTCCCTGGAAGCTATTACACAGAGATGGACAACATTGCCGAGACTTTCCTGAC  
 CTGGCGAGGAGGGTGAAGATTGGACATTCGTTTGAACACGGCCGATGTATGTACTGAAGTT  
 CAGCACTGGGAAAGCGTGAAGCGGCCCGGCTTTGGCTGAATGCAGGCATCCATTCGCCAG  
 AGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACGAGAG  
 GATCCAGCTATCACCTCCATCTTGGAGAAATGGATATTTCTTGTGTGCTGTGGCCAAATCC  
 TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGGGTCCCGAAATC  
 CTGGAAGCTCCTGCATTGGTGTCTGACCCAAATAGAACTGGAACGCTAGTTTTGCAGGAAAG  
 GGAGCCAGCGACAACCCCTTGCTCCGAAGGTACCATGGACCCACGCCAATTCCGAAGTGGA  
 GGTGAAATCAGTGGTAGATTTTCATCCAAAACATGGGAATTTCAAGGGCTTTCATCGACCTGC  
 ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAAGGCCAGCATGCCC  
 GAGGAACTCGACAAGGTGGCGAGGCTTGGCGCCAAAGCTCTGGCTTCTGTGTGCGGCACTGA  
 GTACCAAGTGGGTCCCACCTGCACCATTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG  
 CGTATGACAACGGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCCGGACCTATGGG  
 TTCTCTCTGCCAGCTAACCCAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC  
 CATCATGGAGCATGTGCGGGACAACCTCTACTAGAGCGATGGCTCTGCTGTCTACATTTAT  
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTTCCTACCTGTGTGAG  
 TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCCTGCCCTCTCCAGCCAGCTCCCTGGAGT  
 CGTGTGCTCTGGCGGTGCTCCCTGCAAGAACTGGTTCTGCGAGCCTGCTCAATTTTGGTCTGT  
 CTGTTTTTGATGAGCCCTTTTGTCTGTTTCTCCTCCACCCCTGCTGGCTGGCGGCTGCACCT  
 AGCATCACCCCTTCTGGGTGGCATGTCTCTCTACCTCATTTTAGAACCAAGAACATC  
 TGAGATGATTCTCATCCCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT  
 GTGGGAGACACCACTTTGCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCTCTTAATTTCT  
 TCGAGTCTTCTGGAAAAATATTTCTCTTTGAGCAGCAAACTCTGTAGGGATATCAGTGAAG  
 GTCTCTCCCTCCCTCTCTCTGTTTTTTTTTTTTTTTGTAGACAGAGTTTGTCTTGTGTGCC  
 CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCACAACCTCTGCCTCTGGGTTCAGCA  
 ATTTCTCTGGCTCAGCTCTTGTAGTAGCTTGGTTTTATAGGCGCATGCCACCATGCTGGGCTA  
 ATTTTGTGTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAAGCTGGTCTCAAACCTCCCA  
 ACCTCAGGTGATCTGCCCTCCTTGGCCTCCAGAGTGGCTGGGATTACAGGTGTGAGGCCACTG  
 TGCCGGGCCCTGCCCTCTTTTATAGGCTGAATACAAAGTAGAAGATCACTTCTCTTAC  
 TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTCCCTTTGTTATTACAGTGTG  
 ACCAGGATGGCGGGAGGGGATCTGTGTCACTGTAGTACTGTGCGGAGGAGGCTGGGTGAA  
 GTGACCATCTAAATTTGAGGATGGTGAAATATCCCCATCTGTCTTAATGGGGTTACCTCCT  
 CTTTGCCTTTTGAACCTCACTCAAAGATCTAGGCCCTCATCTTACAGGCTCAATCAATCACTCAT  
 CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCCAATTTGTGCTGTGGTGTATCCTGTGTT  
 TCCTTGTCTGGTTTTGT  
 TCTGTCTATTGTATCTCGGACCACAAGTTTCTAAGTAGAGCAAGAAATTCATCAACCAAGCT  
 GCCTCTTGTGTTTCAATTTCACTCAGCAGCTACCATCTGTCTCTTTGTGTGTGTGTGTGTGT  
 TTGTTTTTTTGTCTTTTACCAACATGTCTTAATCTTAACCTCTGCTGAGGATTTGTGATCA  
 GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 134**

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR  
PVDVLVPSVSLQAFKSFLRSQGLEAYTIEDLQALLDNEDEMQRHNEGQERSNNFNNGAYH  
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRPAPVWLNAGIHSREWI  
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRRLWRKTRSRNPGS  
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPANSEVEVKSVDVFIQKHGKFKGFIDLHSY  
SQLLMYPYGYSVKKAPDAEELDKVARLAALKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD  
NGIKFAFTFELRDTGTYGFLPANQIIPTAEETWLGLKTIMEHVRDNLV

**Signal peptide:**

amino acids 1-16

[illegible]



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# **FIGURE 136**

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE  
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP  
SKDLTLKMGSAFLVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQ GK  
VVDIIQGLDLLTAMVLVNHIFFAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF  
GVDTELNCFVLQMDYKGDVAFFVLPSKGMKRLQEQALSARTLIKWSHSLQKRWIEVFI PRF  
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT  
KFIVRSKDGPSYFTVSEFNRTFLMMITNKATDGILFLGKVENPTKS

**Signal peptide:**

amino acids 1-20

**FIGURE 137**

[illegible]

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## **FIGURE 138**

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATI  
SGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE  
SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS  
TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT  
SNGAGTATNSESSTTSSGASTATNSDSSVTSSGASTATNSESSTTSSGASTATNSESSTSS  
GASTATNSDSSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA  
NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSSTSSEAST  
ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV  
SEAKPGGSLVPWEIFLITLVSVVAAVGLFAGLFFCVRNLSLRNTFNTAVYHHPGLNHGLGP  
GPGGNHGHAPHRPRWSPNWFWRPVSIIAMEMSGRNSGP

### **Signal peptide:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 510-532

# **FIGURE 139**

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC  
 CCAGCAAT**ATGC**CATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC  
 CTGTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG  
 GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGC  
 ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC  
 AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT  
 CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG  
 CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC  
 CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG  
 AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC  
 TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC  
 AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG  
 GGCCTCAGTCAACACGCCTTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA  
 TGCCCT**TAA**ACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTACATCAGCTGAC  
 ATGACCTGGAGGGGTTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGTTGTA

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## **FIGURE 140**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHVNNAAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**Homologous region to circumsporozoite (CS) repeats:**

amino acids 35-225

TC CCGGTC CCCCAGGGCT CCGCCGGGGCCGGCTTGGCAAGGGGACGAGTCACTGGACACTCAGGAAGAGCGGCC  
CGCCGGGGGGGCTGACGCTGCTGCTGACCTACTCACTCAAGGTCGCGAGGGGGGCCGCCCGGGCGACTCG  
GGGGCGGACCGCGGGGCGAGCTCGCCCGGTGAGTTCGCGCGAGGCCACTGACGGCCAGCGCCGGGACCCGCTG  
GCTCTGCTCTCGGCA**ATGCT**CGGCACAGCATGGCGCTGAGGAGCTGGCTCGCCGCCCTATGGGGCGCGCTGCGC  
CTTCGCGACACCGTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCGAGCGCGCGCTCGACCTGGGGCGCTCAGC  
CCCGGACTCAGCTCGTCTGGCTCTGGGCTCTGAGAGCGGGCCATCTCTCAGATTTCGAAGTGAACACTCTCCAACTAC  
ACAGCCCTTCTGCTGACAGGAGTGGCAGGACCTGTACTGTTGGGTGCTGAGAGCGAGGAAGAAACAGCAGTGC  
AGCTTCAAGGGCAGGACCCACAGCGGCATGTCAAATACATCAAGATCTCTCTCGCGCTCAGCGGCAGCTCAG  
CTGTTCACTTGTGGCAGCAGCTCTCAGCCCGATGTGTACTACATCAACATGGAGAATTCACCTTGGCAAG  
GACGAGAAGGGGAATGTCTCTTGGGAATGGCAGGCGGTTGTCCCTTCGACCGAATTTCAAGTCCGACTGCC  
TGTGGTGTGATGGCAGCTCTACATGGAAACATCAGCAGCTTCAAGAGGAATACCGCGGACTCTCGGCGAGC  
CAAGCGTTCGCCCCACCAAGACCGAGACTCCTTCACTGGTCAAGAGCCAGCTTTTGTGGCTCAGCTTAC  
TTTGTCTGAGAGCGTGGGCACTTGAAGGCGATGTATGACAGATCTAAGTTTCTTCGAGGAGACTGCCCAGGAA  
TTTGTGTTCTTGAAGAACATATTGTCCCGATTGCGCCGATTCTGACAGGGCGATGAGGAGTGGAGAGCGGGT  
CTACAGCAGCGCTGGACCTCTCTCTCAAGGCCAGCTGTGTGCTGTCAGCCGCGAGCATGGCTTCCCTTCAAC  
GTGCTCAGGATTTCTTACGCTGAGCCCAAGCCCAAGGAGTGGGTGACACTTTTCTATGGGTTCTTCACT  
TCCGATGGGCACGGGAATACAGAGGCTCTGCCGTTCTGTGTTCTCAATAAGGAATGTGACAGAGAGTTCT  
AGCGGCTCTACAGGAAGGTAAACGCTGAGACAGCAGTGTGGTACCGTGACCCCGGTGCCACACCCCGG  
CTGGAGGCGTCACTCAACAACTGCCCCGGAAGGAAGATCAACTCTCTCTGACCTCCAGACCGCGCTGTCTG  
AACTTCTTCAAGGACCATTTCTGATAGCGGCGAGTTCGAAGCGCATGCTGCTGCTGCGACCCAGGCTCGT  
TACACGCGCTGGCTGTATACACCGCTGCCCTGGCTGCACACACTCATGATGTCTCTTCTGGGCATGTGTGAC  
GGCCGCTTCCAAAGGCTAGCGCTGAGCGTGGCCCGGGGTTGACATCTTAGAGAGCTGCATACTTCTATCGGGA  
CAGCCGCTGCGAAGATTCTCTTGGACACCCACAGGGGGTGTCTGTATCGGCGCTACACTCGGGCGTAGTCTAG  
GTGCCATGGCCAACTGCGAGCTGTACCGAGTCTTGGGAGTGGCTCTGCGCCGGGACCCCTACGTTGCTGTGG  
AGCGGCTCCAGCTCGAAGACGCTCAGCTCTACACCGCTCAGTGTGCCACAGCGCTGGATCCAGGACATCGAG  
GGAGCAGCGCCAAAGCACTTTCAGACGGCTTCTGGTTGTGTCGCCGTTCTTTGTACCAAGAGGGAGAAGCCA  
TGTGAGCAAGTCCAGTTCCAGCCCAACACAGTGAACATTTGGCTCTGCCGCTCTCTCTCAACCTGGGCAACGCA  
CTCTGGATACGCAACGGGGCCCGCTCAATGTCTGGCTCTGCAAGCTGTACCATCGGGGACTGTCTGTG  
GTGGGCAACCAACAGCTGGGGGAGTTCAGTGTCTGTCTAGAGAGGGGCTTCCAGACGCTGTGAGCGAGCTAC  
TGCCACAGAGTGTGTGAGAGCGGGGTGGCAGACAAACAGATAGGGTGGGCAAGTACCGCTATTATTCAGACA  
TCGCGTGTGTAGTGCACCGCTGTGGTGGCAGGGCCAGCTGGGGTGCAGACAGTCTCTACTGGAAGGAGTTCTCTGTG  
ATGTGACGCTTCTTTGTGCTGGCGTGTGCTTCCAGTTTATTCTTCTGCTACCGGACCCGGAACAGATGAAGA  
GTCTTCTTGAAGCAGGGGAATGTGTCAGCGCTGCACCCCAAGACTGCGCTTGGTGTGCTGCCCTTGAGACCGCG  
CCACTCAACCGGCTAGGGGCCCTTAGACACCGCTCGATACAGAGGGTACCACTCCGTGCAGACAGCCCCCG  
GGGGCGCGAGTCTTCACTGAGTCAGAGAAGAGGCCACTCAGCATCAAGACAGCTCTGTGGAGGATATTCCCACTG  
TGCCCGCGGCGGGGTGCGCTTGGCTCGGAGTCTCGTGACTCTGTGCTG**TCAGAGCT**ACTTCCAGAGGAGCT  
TGCCCTTGGCTTCAGGGGCTGTGAATGCTCGGAGAGGGTCAACTGGACCTCCCTTCGCTCTGCTCTCTGTGGAA  
AGCCAGCTGTGTGCGCGGCTTGGGAGCTTGGAGCGAGCTGGCTGTGCTGTCTCAGTCAAGTAGGAGCACTTC  
TACACCCAGACACCAACAGACCGCTGGCCCGAGAGTCTCGTCAACAAATATGGGGCGGCTGCTAGTTTGGTGAA  
CAGTGGCTCTTATGTAACTAGCGCTTTTGTTTAAAAAACATTCAAATGTGAACTAGTAATGAGGGAGAGG  
ATGATGAGCAGATCGACGACACAGCGGTGTCCAGTTTCTATGGCTCCGAGGGGTGCTGGGATGATCCAAATGG  
TTGCTTGAGACAGATTTGGAACCTTCACTCACTGGCTCTTCACTTCCCAATTATCCGCTGCCACCGGCTGC  
CTGTCTCACTCAGTCAATCAGGACAGCTTGGGCTGGTGCGTGTGCTGTCTGCGAGTCAGCCGAGGATGTAGTTG  
TTGTGCGCTGTGCTCCACCACCTCAGGACACGAGGCTAGTTGGCATTCGCGGCTACCAAGTCTCGGGT  
GGACCCACTCTTGAGGCTTTCCAGCTGTATCAGGCTGTGGGCCACAGGAGGACAGGCGAGCTCAGAGAGA  
TTTGTGACAAATTAGCGCTTTCTCTCAGAATTCAAGGAAGAGACTGTGCGCTGCTTCTCCGTTTGTGCTGTA  
GAACCCGTTGCGCCCTTCCCACTTATCACTCTCGCTCTCACTTTGACATCAACACAGGAAGTAATCGCACT  
CTGGTCTCTCCCGAGTCCCGAGTACCTCTCATCTCCGCTCACTTCTCCACTTAAGGATATCAACACTGCC  
AGCACAGGGGCGCTGAATTTATGTGTTTATTATACATTTTATAAGATGCATTTATGTCATTTTATAATAA  
GCTGTGAAGAACTACTGTTTAAAAAATAAAAA

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## **FIGURE 142**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLQPPPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLSRDGRITLYVGAREALFALSSNLSFLPGGEYQELLWGADAEEKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFS PMCTYINMENFTLARDEKGNVLEDDGKGRCP
FDPNFKSTALVVDGELYTGTVSSFQGNDAISRSQSLRPTKTESSLNWLQDPAFVASAYIPE
SLGSLQGDDDDKIYFFFSETGQEFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFPFNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSG
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFKDHFMDGQVR
SRMLLLQPQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVGPRVHII EELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVS LYQP
QLATRPWIQDIEGASAKDLCSASSVSPSFVPTGEKPCEQVQFQPNVTNTLACPLLSNLATR
LWLRNGAPVNASASCHVLPTGDLLLVGTQQLGEFQCWSLEEGFQQIVASYCPEVVEDGVADQ
TDEGGSVPV IISTSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHRNSM
KVFLKQGECA SVHPKTCFVVLPPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKR
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV
```

### **Transmembrane domains:**

amino acids 23-46 (type II), 718-738

**FIGURE 143A**

CTAAGCCGGAGGATGTGCAGCTGCGGCGGGCGGCCGGCTACGAAGAGGACGGGGACAGGCGCCGTGCGAACCGA  
 GCCACCGCAGCCGAGGAGACGGGGCAGGGCGGGGACGGGAGCCCGGACTCGTCTGCGCGCCGCGCTGTCGCCGTCG  
 TGC CGGCCCCCGCTCCCGCGCGCAGCGGGAGGAGCGCGCCGCACTCGCGCCCGAGCGCCCGCTAGCGCGCGC  
 CGGGCATGTGTCCTCTTAAAGCGCAGGGCCGCGCGGGCGGGGCGGGTGTGCGGAACAAGCGCGCGCGCGGG  
 CTTGCGGGCGCGCTCGGGGCGCGCATGCGGCGCGGGCCCGCGCGCGGGCGCGCTGCCCGGGCGGGCCTCG  
 CGCGCTAGGGCGGGCTGGCCTCGTGGGCGGGGCGAGCGGGCTGAGGGCGCGCGGAGGCTCGCGGGCGGGCGG  
 GGGCGCGCGGGCGCGCGGGCGGAGCGCGCGGGC**ATGG**CGCGCGGGCGCGCGCGCTGGCTGACGCTGC  
 TGCTCGGGCTCGTCTGGGCTTCTGCTGCGGCTCGCGGCTCGTCTGCCCGGGGCTTCCGAGCTGAAGCGAGCGG  
 GCCACCGCGCGCGCGCAGCCCCGAGGGCTGCCGCTCCGGGCGAGGCGCGGCTTCCGAGGCCGCGGGCGCGCG  
 GCGATGCGCGCGGGCGCAGCTCTGGCGCGCGGGCTCGGACCCAGATGGGCGCGCGCGGACGAACTTCTCT  
 TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCGTGGCGCTCAGTACATGCACGACCACTACTTGGACA  
 TTCTGGGAAAGTTGAGTTCTTCTCAAGTGAGGGTCTGACACATCTGTACCAATTCAGTAGTGCCACTACGGG  
 GTGTGGAGCACTCTACCGCGCCAGAGAAGTCCCTCATGATGCTCAAGTACATGCACGACCACTACTTGGACA  
 AGTATGAATGGTTATGAGAGCAGATGATGACGTGTACATCAAGAGGAGACCGTCTGGAGAATCTCTGAGGAGTT  
 TGAACAGCAGCGAGCCCTCTTTCTTGGGCGAGCAGGCTGGGCAACCGGAAGAAATGGGAAACTGGCCCTGG  
 AGCCTGGTGAGAACTTCTGATGGGGGGGCTGGCGTGATCATGAGCCGGGAGGTGCTTCGGAGAATGTTGCCGC  
 ACATTTGGCAAGTGTCTCCGGGAGATGTACACCACCATGAGGAGTGGGAAGGTGTCTCCGAGAGGTTTG  
 CAGGGGTGCGAGTGTCTGGTCTTATGAGATGCGGCGAGCTTTTATGAGAATACGAGACGACAAAGGGGT  
 ACATTAGAGATCTCCATAAGCAGTAAATTCACCAAGCTATCACATTACGCCCAACAAACCAACCTACCAAT  
 ACAGGCTCCACAGCTACATGCTGAGCGCAAGATATCCGAGCTCCGCCATCGCACATACAGCTGCACCGGAA  
 TTGCTCTATGAGCAAAATACGACACAGAAATTCACAAAGGAGCTCCAGCTGGGAATCTCTCCCTCTTCA  
 TGAAGTTTACGCCCGCGCAGGAGGAGATTTGGAATGGGAGTTTCTGACTGGAAATATCTGTATTCGGGAG  
 TTGACGGCCAGCCCCCTCGAAGAGCCATGGACTCCGCCAGGAGGAGCTGGAGCAGTTGCTCATGAGCTCA  
 TGGAGATGATCAATGCCAGCGCAAGACAGAGGGCGCATTTGACTTCAAAGAGATCCAGTACGGCTACCGCC  
 GGGTGAACCCATGTCTGGGCTGAGTACATCTGGACCTGCTGCTTGTACAAAGAGCACAAAGGAAGAAAA  
 TGAAGCTCCCTGTGAGGAGCAGCGGTATTTACAGCAGACTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAG  
 TGGATGCACAAGAGTTGGCCACAGAAATCAATCAGGAATCTGGATCTGTCTTCTCTCAACTCCCTGAAGA  
 AGCTCGTCCCTTTACGCTCCCTGGTCCGAGAGTGAGCACAAAGACCCAAAGATAAAAAGATAAATCACTGA  
 TTCTTTGTCTGGGCGTTTCGACATGTTTGTGAGATTTATGGGAACTTTGAGAAGAGCTGTCTTATCCCAAT  
 AGAACGTGAAGCTCGTGGTTTCTGCTTTTCAATCTGATCCCAACCTGACAAGGCCAAACAAGTTGAATCATGA  
 GAGATTACCGCATTAAAGTACCCCTAAAGCCGACATGCAGATTTTGCTGTGTCTGAGAGTTTCAAAGGCCCTGG  
 CCCGGAAGTAGGATCTCCCGAGTTTAAACATGAATCTTGTCTTCTCTGCGAGCTCGACCTCGTGTTTACTA  
 CAGAATCTCTTCAGCATGTGCGAGCAATACAGTTCTGGGCCAACAAATATATTTCTCAATCATCTTCAGCAGT  
 ATGACCCAAAGATGTTTATGATGGGAAGTTCCCAAGTGAACAACATTTTGCTTTACTCAGAAAGATGGCTCT  
 GGAAGAATCATGGGTTTGGCATGCGAGTGATTTATTAAGGAGATCTGTCCGAGTTGGTGCTTGTATGTTCCA  
 TCCAGGCTGGGGGCTGGAGGATGTGGACCTTTTCAACAGGTTGTCCAGGACAGTTTGAAGAGCTTTAGGAGCC  
 AGGAAGTAGGAGTAGTCAGGCTCCACCATCTGTCTTTTGTGATCCCAATCTTGACCCCAACAGTACAAAGTGT  
 GCTTGGGGTCCAAAGCATCGACCTATGGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAATAATGATCCA  
 TTACAGTAAGAAGCAGCAATATAATGGCTCAGTGAGGACAGCG**TAAT**GTCCAGTTGTGCTGGAAAGAGCTTT  
 TAATTAATCTAATTTATTTTCAAATAATTTTGTATGATCAGTTTGAAGTCCGTTGATCAAGATATATTTTAC  
 AAGTGGTTTCTTACATAGGACTCCTTAAAGATTGAGCTTCTGAACAAGAGGTGATCAGTGTGTGGCTTTGA  
 CACATCTCTTGGTGAACATTATGTAGCAGACTGCTTAACTTTGACTTGAATGTACTGATGAACAAACTTT  
 TTTAAAAAATGTTTCTTTTGGAGACTTTGCTCCAGTCCATGCGAGAAACGTGAACTTCGCAAGATTT  
 TATTTGTAAACAAACCTGTACTCTGGTAAATGTTCTGTGTGTATGTTAACTTCCACAGATTTACTTTTGT  
 GTTTGTTTTTTTTTTACAAATGTTTAAAGCCATTTCAATGTTCAAGTGAAGAAATGTGATATA  
 GCTGTTTTCATCATGTCTTCCAGAGAGCTTCCAGAGTTGATCTTCTCTCATGGATCTCTGTCAGGCTGGC  
 CAGGTAGGTTTTTTGTTTGTGTTGTTTGTGTTTGTGAGAGGAGTCTCACTCTGTACCCAGGCTGGAAGT  
 CAGTGGCGCAATCTGGCTCACTTTTAACCTCCACTTCCCTGTTTGTATTTTGTAGTAGAGCGGGGTTTCCACT  
 AGCTGGGATTACGAGCACACACCACGCCAGTAGTTTGTGTTTGTATTTTGTAGTAGAGCGGGGTTTCCACT  
 GCAAGCCGAGCTGGCCAGTGGTTTTAAAGCAGGGGCGTGAAGAGGACAGTGAAGTATGTGCTGTCTCTG  
 TGGATCTTCACTTGGGCTAAATAGACTGGCATTAATTTCAAGAGGATTTGGGCAATTTCTCTCTTGACCCCT  
 CTCTTTAAAGGGTAAATATTAATGTTAGAATGACAAGAGATGAATTTACAAATAATCTGAATGTACAGACT  
 GAAACATGACACATACACCTTAATCAAAAGCTTGGGGAATAATGTTATGGTTTTGTTCTCTTCACTGCTGTG  
 TGTATGTGGGTGGAGATGTTTTCATCTTTCATTAAGTGTGTTTGTATCTGTTTGTATCTGAATACTTTAA  
 TTTATTTAATATCTGTTGTCAGAGCTCTGCCATTTCTGTAGTACCTGTTAGTTAGTATTTATGTGATTCGG  
 GAGTGTGTTAGTCTGTTTTATTTGCGATTAACCGATCTCCAAAGATTTCTTTTGGAAAGCTTTTCCCTCCG



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## **FIGURE 143B**

TTAATTTTATATTCCTTACTGTTTACTAAATATTAAGTGTTCTTTGACAATTTTGGTGCTCATGTGTTTGGG  
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAAGTTAAATTCCTCAGATCAAATGTGCCTTAATAAATTGTT  
TTCATTTAGATTTCAACAGTGATAGACTTGCCATTTTAATACACGTCATTGGAGGGCTGCGTATTGTAAATAG  
CCTGATGCTCATTGGAAAAATAAACCACTGAACAATATTTTCTATTGTACTTTTCGAACCATTTTGTCTCATT  
ATTCTGTTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAACTTAAACACGAAAAAA

# **FIGURE 144**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAYRTWSKTI PGKVQFFSSEG
SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEWFMRADDDVYIKGDRLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCWVSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQRQREE
ILEWEFLTGKYLKYSYAVDGGPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNPYGAEYILDLLLLYKHKHGKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFSLNSLKKLVFPQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVLVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSPDNHFAFT
QKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLEDDVDFNKKVQAGLKTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMCGLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA
```

## **Signal peptide:**

amino acids 1-23

**FIGURE 145**

GGACAACCGTTGCTGGGTGTCACAGGCGCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC  
TTTCGGCCTTGAGGTTCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT  
ACGGACGACGCCTATGAAGCCCTTAGTCCCTCTAGTTGCGCTTTTGCTATGGCCTTCGCTCG  
TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA  
CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATC  
TAACCTCTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTA  
CACATGGAGACGCTTCAACTGAGAATGATGTTTAAACCAATCCTATCAGTGAAGAACTACA  
ACTTTCCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCC  
ATTCTGGTCGATCAAACCAAACATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG  
AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG  
TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTAC  
CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT  
CAGGTGAAACTGCGATAGAAAAACCCGAAGAGTTTGAAAGCACCCAGAGAGTTGGAATAAT  
GATGACATTTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCTTAGTGA  
CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC  
TTGCTCTAGCAGCAGCAGACAATAAATAAAAACAATGTATAAGTCCCAGTTATTGCCA  
GTAGACGAACAAGTAATAAAATTGATGACATCGAACTGTTATTAACATGCTGTGTAATTC  
TAGATCTAAACTCTATGAATATTTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAG  
CTGTACAGTATTCAATACATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA  
AAAGTTTATTAACAATAATATAAAAAATTTTAAACCTACTTGATATTCATAACAAAGCTGA  
TTTAAGCAAACCTGCATTTTTCACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTAT  
AAAAATATTTTCTATTGTAGTCAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACA  
ATTTTCATATGCACTAAAAACCTAATTTAAATAAAATTTTGTTTCAGGAAAAA

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## **FIGURE 146**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864

><subunit 1 of 1, 350 aa, 1 stop .

><MW: 39003, pI: 5.59, NX(S/T): 1

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRVSPSGEFGREKKSNSPK  
 HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTFPTGGFTPEIGKKKHTESTPFWSI  
 KPNNVSIVLHAEPEYIENEEPEPEPEPAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK  
 STGIEISTESEDVQQLSGETAIEKPEEFKGHPESWNNDDILKKILDINSVQQALLSDTSNP  
 AYREDIEASKDHLKRSLALAAAAEHKLKTMYSQLLFVGRTSNKIDDIETVINMLCNSRSKL  
 YEYLDIKCVPPMEMREKAATVFNTLKNMCRSRRVTALLKVY

**Signal peptide:**

amino acids 1-19

**FIGURE 147**

GGGCTCGAGCGGCTCTAGTGAAGAGCCTCTCACGGCTCCTGCGCCTGAGACAGCTGCGCTG  
ACCTCCAAATCATCCATCAACCCCTGCTGCTCATCTGTTTTATGATGTGAGATCAACCCACA  
GGAATATCCATGGCTTTTGTGCTCATTTTGTGCTTCAGTTTCTACGAGCTGGTGTGAGGACA  
GTGGAAGATCATCGGACGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT  
CTTGCTCCCTCTTCTCTGACGACCGTGCAGAGGCTATGGAAGTGCGGTCTTTCAGGAATCAG  
TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGAATCTAAGCAATGTCACCA  
GTATCGAGGGGAAGACTAGGATTTGTGAGGACTCCATTGCGAGGGGGGCGTCTCTCTAAGG  
TAAAAAATCATCCCTCGGACTCATCGGCTGTATGGGTGCTGGTTTCAGTTCGCAATTTAC  
GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCTCTCATTTCAT  
CGTGGGATATGTTGACGGAGGTATCCAGTTACTTGCTGCTCTCAGGCTGGTTCCCCCGAC  
CCACAGCCAAGTGAAAGGTCACAGAGCAAGGATTTGTCTCAGACTCAGAGCAATGCA  
GATGGGTACAGCCTGTATGATGTGAGATCTCCATTTATAGTCAGGAAATGCTGGGAGCAT  
ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGAAATCCAAGGTATTGATAGGAG  
AGACGTTTTTTCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACTGGGTTACTCTGTGGT  
GCCCTGTGTGGTGTGTGATCGGGGATGATAATGTTTTTCTCAAATCCAAGGGGAAATCCA  
GGCGAAGTGGACTGGAGAAGAAAGCACGGACAGGAGCAAGTATGAGAGAGCGCCGGAAACAG  
CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTTCTGCGTTTCTGATCTGAAA  
ACTGTAAACCATAGAAAAGCTCCCCAGGAGTGCTCAGACTCTGAGAAGAGATTTACAAGAA  
GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGGACACTTACTGGGAGGTGGACGTGGGAC  
AAATGTAGGGTGGTATGTGGGAGTGTGTGCGGATGACGTACAGAGGGGGGAAGAACATGTG  
ACTTTGCTTCCCAAAATGGGTATTTGGGTCTCAGACTGACACAGCAACATTTGTATTTCAC  
ATTCATATCCCCATTTTATCAGCCTCCCCCAGCAACCCCTCTACACAGTATAGGGGTCTTCC  
TGGACTATGAGGGTGGACCATCTCTCTTCAATACAAATGACACGCTGCTTTATTAACC  
CTGCTGACATGTCAAGTTTGAAGGCTTGTGTAGACCTTATCCAGCATGCGATGTATACGA  
GGAAAGGGGAGCTCCCAATTCATATGTCCAGTGTCTCTGGGAGTGAAGCAGAGAGACCTGT  
CTTAAAGGGCCCCACACCAAGCAGCCAGACAGCCAGGAGAGTGTCTCCGACAGGTGGC  
CCCAGTTCTCTCTCCGGAGCCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGC  
TGAGGTTCTTCTGCCCCTGAGCCCTGCAGCAGCGGACGTCAAGCTTCCAGATGAGGGGGAT  
TGCCCTGACCCTTGGGAGTCAGAAGCATGGCTGCGCTGAGTGGGGAGCGGAATAGACTCA  
CATTAGGTTTAGTTTGTGTGAAACTCATCCAGTAAAGCATCTTGAACAGTACAACCTCC  
CAGGCTCCTCATTTGCTAGTCCAGGACGATTCCTGTCCTCAGAGTGAGATTTAAGAGC  
CAACGAATGTGAATCATGCTTGCAGGTTTGAAGGGCACAGTGTTTGTCAATGATGTGTTTTTA  
TATTATACATTTTCCCACATAAATCTTGTGCTTATTCACATTAATTTACTTTCTCTCTA  
TACCAATACACCATGGGAATAGTTATTGAACCTGCTTTGTGAGGCTCAAGAATAAAGAG  
GAGGTAGGATTTTCTACTGATTTATAAGCCAGCATTACCTGATACCAAAACACGGCAAG  
AAACACAGAAGAGGAGGAAGGAAACTACAGGTCCATCTCCCTCATTAACACAGACACAAAA  
TTCTAAATAAAATTTTAAACAATTAACATAAACAAATATTTAAGATGATATATAACTACT  
CAGTGTGGTTTGTCCCAAAATGACAGATGGTTTGAATTTTAAATATTAACACAGGTGAAT  
CAGCATATTAATAAGTAAAAAGGAAACCAATAAAAAA

**FIGURE 148**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALC
GVVMGMIIVFFKSKGKIQAELDWRKHGQAEIRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS
PNNGYWVLRRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLTL
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG
```

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

# **FIGURE 149**

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTA  
 GGAAAAGAGTTTGTGGGAACCTGGGTTATCGGCCCTCGTCATCTTCATATCCCTGATTTGTC  
 CTGGCAGTGTGCATTGGACTACTGTTTCATTATGTGAGATATAATCAAAAAGAACCTACAA  
 TTACTATAGCACATTGTCATTTACAACCTGACAACTATATGCTGAGTTTGGCAGAGAGGCTT  
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGA AAAATGCATTTTATAAA  
 TCTCCATTAAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG  
 AGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAG  
 ATAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA  
 GATCCTCACTCAGTTAAAATTA AAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA  
 TTGCTGCGGAACACGAAGAAGTAAAATCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAG  
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT  
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGTCTGCTCATGTTTACACATATAA  
 GAACCTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG  
 GTCTCCGGAGAATAATTGTCCATGAAAATACAAACACCCATCACATGACTATGATATTTCT  
 CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA  
 TGCATCCTATGAGTTTCAACAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACGAAAA  
 ATGATGGTTACAGTCAAATCATCTTCGACAGCAGAGGTGACTCTCATAGAGCTACAAC  
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT  
 AGAAGGAAAAACAGATGCATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTA  
 GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCAACAAG  
 CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCTA  
 AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTTGGGTGTGGAGGCCATT  
 TTTAGAGATACAGAAATGGAGAAGACTTGCAAAACAGCTAGATTGACTGATCTCAATAAAC  
 TGTGTTGCTTGATGCATGTATTTTCTCCAGCTCTGTTCCGCACGTAAAGCATCTCTGCTCTG  
 CCAGATCAACTCTGTCTATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA  
 ATACAATATTACATTACAGCCTGTATTCTATTTGTTCTCTAGAAGTTTTGTGAGAATTTTGAC  
 TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTC  
 AGCTCCTCTCATTTACAGCAATATCCATTTTCAAGGTGCAGAACAGGAGTGAAAGAAAATA  
 TAAGAAGAAAAAATCCCTACATTTTATTTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT  
 GGAATATTAGAAATGATCATATTCTATTATGAAAGTCAAGCAAGACAGCAGAATACCAATC  
 ACTTCATCATTTAGGAAGTATGGGAACCTAAGTTAAGGAAGTCCAGAAAGAACCAAGATATA  
 TCCTTATTTTTCATTTCCAAACAACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG  
 ACCTATAATAATTATACAACTTCATGCAATGTACTGTTCTAAGCAAATTAAGCAAATAT  
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

## **FIGURE 150**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTNYNSTLSFTTD
KLYAEFGREASNNFTMSQRLESMVKNAFYKSPLEEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPYTNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNLHRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIYWLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKGTI
```

### **Transmembrane domain:**

amino acids 21-40 (type II)



## FIGURE 151

GTCGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA  
CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTCAGCTGGTGGATTCCCG  
CTGCATCAAGGCCCTACCCACTGTCTCC**ATG**CTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC  
CGTGACCTTCTTGGTTCCAGAGCTCAGCCCTTGGCCCCCAAGACTTTGAAGAAGAGGAGG  
CAGATGAGACTGAGACGGCGTGGCCGCCCTTGGCCGCTGTCCCTGCGACTACGACCACTGC  
CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGTCGGGCCGGCGGCTGCCTGTGCC  
AGGACTCTCCAGCCCCGCCAGCCGCCGACCGCCGCGCATGGGAGAAGTGCGCATTGCGG  
CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCGGTCTCTCCACTACTGG  
CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCGCTGAACGCTACGGTCCG  
CAGAGCCGAACGAAGGGGCTGAAGCCAGGGGGCATTATGTGCTTTGCGTAGTGGCCGCTA  
ACGAGGCCGGGGCAAGCCGCGTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC  
CCTGCCTTCGGGCCCTTGACCGCCTTGCGGTGCGGCCAACCCCCGCACTCTGGTCCACGC  
GGCCGTGCGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT  
GCCTGCGGATCGCTGGGGCTGCCCGCGCCGAGCCGCCGCCGAGCCGCGCAGGGGCGCTC**TGA**  
AAGGGGCTTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCG  
GGAAAGAGGAAAACCCGCTGCCTCAGGGAGGGCTGGACGGCAGCTGGGAGCCAGCCCCAG  
GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGTA  
GGCGCTTTGTTTCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCAATTTTTTTTTTA  
AGCGGCCAGATAATAAATAATGTAACCTTTGCGGTTAAAAAAAAAAAAAAAAAAAA

**FIGURE 152**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAPQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE
LQRVGPAACLCPLGSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLLDGSEA
AQKGPPLNATVRRRAELKGLKPGGIYVVCVVAANEAGASRVPAAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVAHAVGVGTALALLSCAALVWHFCLRDRCPRRAAARAAGAL
```

**Important features of the protein:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 194-220

**N-glycosylation site.**

amino acids 132-135

**FIGURE 153**

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC  
 CTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCAGGG  
 CCCAGCGCCGACGATCGCTGCGGTTTTGCCCTTGGGACTAGGATGTGGTGAAGGATGGGGC  
 TTCTCCCTTACGGGGCTCACAAATGGCCAGAGAAGATCCGTTGAAGTGTCTGCGCTGCTGCTGCT  
 CTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGA  
 TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC  
 ATTTTGACTTACTTTCCTGTGGTTCATCGGTGCATGATTGCTGTTTGTCTGTTTTCCTTATCAT  
 TGTGGGAGTTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGGATGGTACT  
 TTGGAAGTTTGTCTGTCATTTTCTGTGTAGAAGTGGCTTGTGGCCTTTGGACATATGAACAG  
 GAACCTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTA  
 TGGATTACCTAGATATCGGTGGCTTACTATGCTTGGAAATTTTTTCAGAGAGAGTTTAAAT  
 GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAATGACAGAGATGGACTGGCCCCCAGAT  
 TCCTGCTGTGTAGAGAATCCCAGGATGTTCCAAACAGGCCCCACAGGAAGATCTCAGTGA  
 CCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCTTTTGTAGAGGAACCAACAAGTGC  
 AGGTGCTGAGGTTTTCTGGGAATCTCCATTGGGGTGACACAATCTCGGCCATGATTCTCACC  
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCTCGGCACAGACCAATGATGTC  
 CTTGAAGAATGACAACCTCTCAGCACCTGTCTATGCTCCCTCAGTAGAAGTGTGAAACCAAGCC  
 TGTCAAGAATCTTTGAACACACATCCATGGCAACAGCTTTAATACACACTTTGAGATGGAG  
 GAGTTATAAAAAGAAAATGTCACAGAAGAAAACCAACAAGTGTGTTTATTGGACTTGTGAATT  
 TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACA  
 CTTAAGCATATACTATTTCTATGCTTTAAATGAGGATGAAAAAGTTTCATGCTATAAGTCAC  
 CACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC  
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGTATTAGCATTTT  
 CGCATCCATGCAACGAGTCACATATGGTGGGACTGGAGCCATGATAAAGTTGATTACTT  
 CTACCAACTAGTATATAAAGTACTAATTAATGCTAACATAGGAAGTTAGAAAATACTAATA  
 ACTTTTATTACTCAGCGCTCTATTCTTCTGATGCTAAATAAATATATATCAGAAAACCTTC  
 AATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCCTTAAAA  
 GAGCAAGCTAACACATTTGCTTAAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTAA  
 TCTGTATAATTCGATTTTCACTTTGATTAATGTTAAGAAATAACCATATGAAAAAGGAAA  
 ATTTGCTCTGTATAGCATCATTATTTTAGCCTTTCTGTTAATAAAGCTTTACTATTCTGT  
 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAATAATA  
 CCAGTGTGATACATAGGAATCATTATTCAGAAATGTAGTCTGGTCTTTAGGAAGTATTAAATA  
 GAAATTTTGCACATAACTTAGTTGATTCAGAAAGGACTTGATGCTGTTTTCTCCAAATG  
 AAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGGCCTTCTCCAAACAAGAA  
 CCAATAGTCTCCAAGTCAATATAAATCTACAGAAAATAGTGTCTTTTTCTCCAGAAAAAT  
 GCTGTGTAGAATCAATTAACATGTGACAAATTTAGAGATCTTTGTTTATTTTCACTGATTA  
 ATATACTGTGGCAAATACACAGATATTAAATTTTTTACAGAGTATAGTATATTATTTT  
 GAAATGGGAAAAGTGCATTTTACTGATTTTGTGATTTTGTGTTATTTCTCAGAAATATGGAA  
 AGAAAAATAAAATGTGTCAATAAAATTTTCTAGAGAGTAA

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## **FIGURE 154**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWVWYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF
PGCSKQAHQEDLSLDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDSQHLSCPSVELLKPSSLRIFEHTSMANSFNTHFEMEEL
```

### **Signal peptide:**

amino acids 1-33

### **Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

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## FIGURE 155

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCCTGCCCTGCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGTACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACCCGATCCCCATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTGTCTCATCAAGGTGATCTGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCAGGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCCGAAGGGCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCACAGGAACTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAGACGGCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA TGTGTGTTGAAATCACAGAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTCTCTCAGGCTCCCTGGTCTCCCTGCACCTGTCTGTGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGGAGGAGGCCCTGTGTGGATTCTTGGCCTTGGCAGGTGAGCATCCAGTACGA CAAACAGCAGCTGTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTCTCAGGCACAGTCAGGCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGCTCAGTCCA GTTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCAACCAGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGTGTGGACACCTGCCAGGTGACAGTGGTGGGCCCTGATGTATACCAATCTGACCAAGTGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGGGGGCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTGTAATGCTGTCTGCCCTTTGCACTGCTGGGAGCCGCTTCCTTCTCTGCCCTGCCCACTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCTTGGGTACACCCCTCTGCCACAGCCTCAGCATTCTTGGAGCAGCAAAGGGCCTCAATTCTGTGAAGAGACCTCGCAGCCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGTCTCCAGCATCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA GGAACCTTTCACACTACTGTAATGGAAGCAGGCTGTCTTGTAAAGGCCAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTACCCTATCCCCAAGCCTA CTAGAGCAAGAAACAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCTACTGTTGTATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAAAAA

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## **FIGURE 156**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVVKPLRKPRIPMETFRKVGIPIIIIALLSLASIIIVVLIKVILDKYYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAETACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNRSSGCLSGSLVSL
HCLACGKSLKTPRVVGGEASVDSWPWQVSIQYDKQHVCSSILDPHWLTAACFRKHTDV
FNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNIDIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAPIPE
GGVDTCQGDSSGGLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
```

### **Transmembrane domain:**

amino acids 32-53 (typeII)

## FIGURE 157

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAACGACAGCGGCATCCCCAGGCTCCAG  
AGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCGACCCCTGGGCCCTGGACCCTGGAGCCCTCCTGGGCC  
TTTTCTCTTCCAACCTGCTTCAGTCTGCTGCTGCCGACGACGACCGGGGGGAGGGGGGAGGGGCCCATGCCCA  
GGGTGAGATCTATGCAAGGAGTAACCTAGGGCATTAGCTTCTTCCACCAGAGGGCCCTCCAGGATTTTGACA  
CTCTGCTCCTGAGTGGTATGGAAATACTCTCTACGTGGGGCTCGAAGACCAATCTTGCCCTTGGATATGCCAGG  
ATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCCTTTA  
AGAAGAAGAGCAATGAGACACAGTGTTCACCTTCATCCGTGCTCTGGTTCTTACAATGTACCCATCTCTACA  
CCTGGGCCACCTTCGCTTCAGCCCTGCTGTACCTTCATTGAACCTCAAGATTCTACCTGTTGCCCATCTCGG  
AGGACAAGGTCATGGAGGGAAGGCCAAAGCCCTTTGACCCGCTCAAGCATACGGCTGTCTTGGTGGATG  
GGATGCTCTATTTCTGGTACTATGAACAACCTCCTGGGAGTGAGCCCATCTGATGCGCACACTGGGATCCCAGC  
CTGTCTCAAGACCGACAACCTTCCTCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCC  
AGGTCGTCTACTTCTTCTCGAGGAGACGCCAGCAGGTTTGAATCTTTGAGAGGCTCCACACATCGCGGGTGG  
CTAGAGCTTTCGAAGAATGACGTGGCGGCGAAGCTGCTGCAAGAGAGTGGCCACCTTCTGAAGGCCAGC  
TGCTCTGCACCCAGCGGGGAGCTGCCCTTCAACGTATCCGCCACGCGGTCTGCTCCCCGCGATTCTCCCA  
CAGCTCCCCACATCTACGACGTCTTCACCTCCAGTGGCAGGTTGGCGGGACAGGAGCTCTCGGGTTTGTGCT  
TCTCTCTTGGACATTGAACGTGTCTTAAAGGGAAATACAAAGAGTTGAACAAAGAAATTCACGCTGGACATA  
CTTAGAGTGGCCCTGAGGACCAACCGCCGAGGAGTGTCTGAGCGCCCTCCTCTGATAAGGCCCTGACCT  
TCATGAAGGACCATTTCTGATGGATGAGCAAGTGGTGGGACGCCCCGCTGCTGGTGAATCTGCGCTGGAGTATA  
CAGGGCTTGACGTGGAGACAGCCAGGGCCTTGATGGGACAGCCATCTTGTATGTACCTGGGAACCCACAG  
GGTGGCTCCACAAGGCTGTGGTAAGTGGGACAGCAGTGTCTCATCTGGTGAAGAGATTGAGCTGTTCCTGACC  
CTTAGAGCTTTCGAAGTGTGAGGCCCAACCCAGGCTGCAAGTGTGTTGAGGCTTCTCAGGAGGTGTCTGGA  
GGGTGCCCGAGCAACTGTAGTGCTATGAGAGCTGTGTGAGCTGTGTCTTGGCCGGGACCCCATGTGCT  
GGGACCTGAGTCCGAACCTGTGCTCTGTCTGCCCAACCTGAACCTCTGGAAGCAGGACATGAGAGCGG  
GGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCGCAAAATCATT  
AAGAAGTCTTGCTGTCCCAACTCCATCTGGAGCTCCCTGCCCCACCTGTACGCTTGGCCTCTTATTATT  
GGAGTCATGGCCAGCAGCAGTCCGAAGCCTCTTCACTGTCTACAATGGCTCCCTCTTGTGATGATGAGG  
ATGGAGTTGGGGTCTCTACAGTGTGGGCAACTGAGAATGGCTTTTCATACCTGTGATCTCTACTGGGTGG  
ACAGCCAGGACAGACCTTGGCCCTGGATCCTGAATGGCAGGACATCCCCGGGAGCATGTGAAGGTCCCGTTGA  
CCAGGCTCAGTGGTGGGGCCGCTTGGCTGCCAGCAGTCTACTGGCCCACTTTGTCACTGTCACTGTCTCT  
TTGCTTAGTGCTTTAGGAGCCCTCATCTCTCTGTCCTTCCCATTGAGAGCTACCGGCTCGGGCTCAGGAG  
TTAGGGCTGTGAGACCTGCGCCCTGGGGAGAAGGCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAG  
AATGACAGGACCTTGCCAGTGATGTGGACGCTGACAAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA  
CAGGCCGGGGCTGCGGTGAGGCACCTTGGCCATGTGTGGTGGGCGGCCAAGCAGACCCCTGACTAGGATGACAG  
CAGCACAAAGACACCTTTCTCCCTTGAGAGGAGCTTCTGCTACTCTGAGGACATGATGACACCAACACTCCCT  
ATGCACAGCAGTCTGCTCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGCTAC  
CCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCTC  
CAGAAACACAGTGTTCAGAGACCCATAAAAAACCTGCCTGTCCCAGGACCTATGTAATGAACACCAACATC  
TAAACAATCATATGCTTAACTGCCACTCTGGGAAACCTCCACTGAAAGCTGGCCCTTTGAGACACCAACACTCCCT  
TCTCCAGGGTCATGCAGGGATCTGCTCCCTCTGCTTCCCTTACAGTCTGTGACCGCTGACTCCCGAGGAATC  
TTTCTGAAAGCTGACCACTTTCTTCTGCTTCAGTTGGGGCAGACTGTGATCCCTTCTGCTCCGGCAGAAATG  
CAGGGGTAATCTGAGCCTTCTTACTCCTTTACCTAGCTGACCCCTTCACTCTCCCCCTCCCTTTTCTTTGT  
TTTGGGATTACGAAACCTGCTTGTCAGAGACTGTTATTTTATTAATAATATAAGGCTTAAAAAA

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# **FIGURE 158**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSLLGLFLFQLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQ
DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAAKHHTA
VLVDGMLYSGMTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFFE
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRTWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGSLSHKAVVSGDSSAHLVEEIQLPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
HFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVDADNNCLGTEVA
```

## **Signal peptide:**

amino acids 1-30

## **Transmembrane domains:**

amino acids 136-156, 222-247, 474-490, 685-704



**FIGURE 159**

AGGGTCCCCTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAAG  
 TGAG**CATG**GCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCCTTCTCCCTGGGGTCTTGCTC  
 TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGGA  
 CCGGCTTTCTCAGATTCTTCAAGATCACGGTCATAATGTACCATTGTTAAACCACAAAAGAG  
 GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA  
 CCTGAAGATCATCAAAGAAATTTAAAAAGAGTTTGATTTCCTTCTGGAAGAACTTTAGG  
 TGGCAGAGGAAAATTTGAAAACCTTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC  
 ATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAAATGAGAACTTCGACATGGTGATA  
 GTTGAAACTTTTGACTACTGTCCCTTCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGC  
 CATTCTTCCACTTCATTGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCC  
 CAGTATCCGTTCCCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTG  
 ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA  
 GGAACATTTACAGAAGGCTCTAGGCCAGTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT  
 GGTTCACTAACTCTGACTTTGGCTTTGATTTTGTCTGACCTCTGCTTCCCAACACTGTTTAT  
 GTTGAGGCTTGATGGA AAAACCTATTAAACCAAGTACCACAAGACTTGGAGAACTTCATTGC  
 CAAGTTTGGGACTCTGGTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCCAGA  
 ATCCGGAATCTTCAAGGAGATGAACAAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG  
 AAGTGTCACTGTTCTCATTTGGGCCAAAGATGTCCACCTGGCTGCAAAATGTGAAAATTTGGA  
 CTGGCTTCTCAGAGTGACCTCTGGCTCACCCAAGCATCCGCTGTGTTTGTCAACCCACGGCG  
 GGCAGAAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT  
 GGAGACCAGCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCCTATTACAGTT  
 AAAGAAGTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT  
 ACAAGTCCGCGGCAGTGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAG  
 CGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGGACGCACCTCAAGCCCTA  
 TGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTCCAGCTTTTTGTGTTTCTGCTGGGGC  
 TCACCTCTGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT  
 GGGGCCAGAAAGGTGAAGGAGACAT**TAA**GGCCAGGTGCAGCTTGGCGGGGTCTGTTTGGTGG  
 GCGATGTCAACATTTCTAGGGAGCTTCCCACTAGTTCTGCGCAGCCCCATTCTCTAGTCCCTC  
 TAGTTATCTCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCTTCCACTTGC  
 TAATTTTGTACAAATTCATCCTTACTAGCTCCTGCTGCTAGCAGAAATCTTCCAGTCCT  
 CTTGTCCCTCCTTTGTTTGGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG  
 GACCACTGACCCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTCCGAA  
 TCACACCCCTGACTCTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCTCTGCCCC  
 TACTATCTATCATGGAAATAACATCCAGAAAGACCTTGCATATTCTTTCAGTTTCTGTTTT  
 TGTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTACAGGGC  
 CGGACACAGGCTCACAGGTCTCCACATTTGGTCCCTGTCTCTGGTGGCCACAGTGAGCTCCT  
 TCTTGGCTGACAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAAAATAAAAGTTTACA  
 CGGTATCTCTCCCCAACCTCACTAA

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## **FIGURE 160**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169
><subunit 1 of 1, 523 aa, 1 stop
><MW: 59581, pI: 8.68, NX(S/T): 1
MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKGRP
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGGKPFVAILSTSFGSLEFGLPIPLSYVPV
FRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAEWLF
INSDFAFDFAFPLLPNTVYVGGLMKPIKPVQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNAFAHLPQGVIVKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ
NSIMEAIQHGVPVMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFPQPPWHEQYLFDFVFVFLGLT
LGTWLWLCGKLLGMAVWWLRGARKVKET
```

### **Signal peptide:**

amino acids 1-19

### **Transmembrane domain:**

amino acids 483-504

**FIGURE 161**

GGGCTGTTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT  
 GCCTCTGGCATATGCACACACTCACACATTTCTGTACACCCGTCACACACATACCATTGTT  
 CTCCATCCCCCAGGTCAGCCCTCAGTGCTGTCCATCCAGCAGGGCTACCTGGAAGCTCT  
 GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCA  
 ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT  
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTAGCGAGCCTAGAGAGGGC  
 AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAACAGAAAGAGGGGCGAGA  
 AGACCGGGGCACTTGTGGGTTGCAGAGCCCTTCAGCCATGTGTGGGAGCCAAAGCCACACTGGC  
 TACCAGGTCCTACACAGTCCCGGGGTGCCCTTGCTTCTGGTGCTTCTGGCCCTGGGGGCC  
 GGGTGGGCCAGGAGGGGTTCAGAGCCCGTCTGCTGGAGGGGAGTGCCCTGGTGGTCTGTGA  
 GCCTGGCCGAGCTGCTGCAGGGGGCCCGGGGAGCAGCCCTGGGAGAGGACCCCTGGGC  
 GAGTGGCATTGTCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC  
 ACCAGTGGGGCCATCTACTTCGACCAGGTCTTGGTGAACGAGGGCGGTGGCTTTGACCGGCC  
 CTCTGGCTCCTTCGTAGCCCCGTCCGGGGGTGTCTACAGCTTCGGGTCCATGTGGTGAAGG  
 TGTACAACCGCAAACCTCCAGGTGAGCCTGATGCTGAACAGCTGGCCGTGTCTCTCAGCC  
 TTTGCAATGATCCTGAGCTGACCCGGGAGGCAGCCACAGCTCTGTGCTACTGCCCTTGA  
 CCCTGGGACCGAGTGTCTCTGCGCCTGCGTTCGGGGGAATCTACTGGTGGTTGGAAATACT  
 CAAGTTTCTCTGGCTTCCTCATCTTCCCTCTCTGAAGGACCCAAGTCTTTCAAGCACAAGAAT  
 CCAGCCCCTGACAACCTTTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG  
 ACTCCTCTGGCTCCTATCCCACCTCTTTGATGGGACCTGTGCCAAACACCCAAGTTTAA  
 GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCCTTCCACCCACCCACCCCAAGTTACC  
 CTCCCAGCCACCTGCTGCATCTGTTCCTGCCCTGACGCCCTAGGATCAGGGCAAGGTTTGGCA  
 AGAAGGAAGATCTGCACTACTTTGCGGCCCTCTGCTCCTCCGGTTCCTCCACCCAGCTTCCT  
 GCTCAATGCTGATCAGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCACAGGAGGCCAG  
 ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCTGTGAGGAAGCCAGCATCACGGATC  
 TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC  
 AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGTTGATTG  
 TCTAGACTGAACATGGTACACATTTCTGCATGTATAGCAGAGCAGCCAGGATAGCAATCCT  
 GGCTGCTCCTTCTATGCTGGATCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG  
 GGTGAGTGTGTTTGTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG  
 ACCATGGAAAACATCGATAACCATGCATCCTCTTGCTTGGCCACCTCCTGAACTGCTCCAC  
 CTTTGAAGTTTGAACCTTTAGTCCCTCCACACTCTGACTGCTGCTCCCTTCCTCCCACTCTC  
 TCATGAGTTATCTTCACTGTACCTGTTCACGATATCCCCACATCTCTCTTCTCTCTGAT  
 CTGTGCTGCTTATTCTCTCTCTTAGGCTTCTTATTACCTGGGATTCATGATTCATCTCTT  
 CAGACCCTCTCCTGCCAGTATGCTAAACCTCCCTCTCTCTTTCTTATCCCGCTGTCCCAT  
 GGCCACGCTGGATGAATCTATCAATAAAACAACTAGAGAAATGGTGGTCAGTGAGACACTAT  
 AGAATTACTAAGGAGAAGATGCCCTCTGGAGTTGGATCGGTTTACAGGTACAAGTAGGTA  
 TGTTGCAGAGGAAAATAAATATCAAACCTGTATACTAAATTAATAA

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## **FIGURE 162**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop .

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVLLLEGECLEVCEPGRAAAGGPGGA  
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY  
SFRFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRG  
NLLGGWKYSSFSGLIFPL

**Signal peptide:**

amino acids 1-32

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**FIGURE 164**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop .
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIADVLYFTWLVFDWNTPKKGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHHPHGIMGLAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLRREYLMSSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM
PGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGWSGRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYEALVKLFDK
HKTKFGLPETEVLEVN
```

**Important features of the protein:****Transmembrane domain:**

amino acids 76-97

**N-glycosylation sites.**

amino acids 60-63, 173-176, 228-231

**N-myristoylation sites.**

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

## FIGURE 165

GGGCGCGGGATGGGGCGCGGGGCGCGCGGCGCCGACTCGCTGAGGCCCGACGACGAGGGCCGGGCGGGCCCGGCGG  
GGGCCGAGGAGCGCGCGGCGAGAGCGGGGCGCGGAGGCGACGCCGGGACGCCCGCGACGAGCAGGTGGCG  
CGGCTGCAAGCTTGTCCAGCGGAAGCCCTGAGGGCAGCTGTCCCACTGGCTCTGCTGACCTTGTGGCTTGGG  
CGGCTCTCTCAGCGAGGGCCGTCACCCGCTCTGAGCAGCGCCATGGGCTCTGCTGCTCTCTCTGAGAGCCCA  
GTTCTGCTGCTCAGCTGCTGGTGGCTTGTCTCTGCTGAGTGGTCTGCTGACCTCTGCTCAGCTGTGAC  
GCTGGCGCTCTGGCCGCTCAGCAAGCAGCTCTACCGCGGCTCAACTGCCGCTCGCTACTACTCTGGAGCCA  
ACTGGTCATGCTGCTGGAGTGGTGGTCTGCACGAGTGTACACTGTTACAGGACGAGGCGACGGTAGAGCGCTT  
TGGGAAGGAGCAGCAGTCATCATCTCAACCACAACCTTCGAGATCGACTTCTCTGTGGGTGGACCATGTGTGA  
CGCTTCGGAGTGTCTGGGAGCTCCAAGTCTCGTCAAGGAGCTGCTGTACGCTGCCCTGCTCAGCTGTGAC  
GTGGTACTTCTGAGATTTGTGTCTGCAAGCGGAAGTGGGAGGAGGACCGGACACCGTGGTGAAGGCTGAG  
GCGCTGTGCGACTACCCGAGTACATGTGGTTCTCTCTGACTGCGAGGGGACGCGCTTACGGAGACCAAGCA  
CCGCTTAGCTGAGGTGGCGGCTGCTAAGGGGCTCTCTGCTCAAGTACCACCTGCTGCCGGGACCAAGG  
CTTCACCAACCGCAGTCAAGTGCTCCGGGGACAGTCGACGCTGTCTATGATGAACCTGAACCTCAGAGGAAA  
CAAGAACCCTCCCTGCTGGGATCCTCTACGGGAAGAAGTACGAGCGGACATGTGCGTGAGGAGATTTCTCT  
GGAAGACATCCCGTGGATGAAAGGAAGCAGCTCAGTGGCTTCATAAAGTGTACGAGGAGAGGAGCGGCTCCA  
GGAGATATATAATCAGAAGGACATGTTTCCAGGGGAGCAGTTTAAAGCTGCCCGGAGGCGCTGGACCTCTGAA  
CTTCTGCTGCTGGGCGGACCTTCTCAGTCTCCCTCTCAGTCTTCTGAGTCTTGGGACGCGGATCAC  
TCTCTGATCTGACTTCTTGGGTTTGTGGGAGCAGCTTCTTGGAGTTCGACAGCTGATAGGAGATCGCT  
TGAACTGGGAGTGGAGATTGCACTGAGCTGAGATGGCATCACTGTACTCCAGCTTAGGCAACAGAGCAGACT  
CAGTCTCAAAAAAAAAAAAAACAAAAAACCCAGAAATTTGGAGTTGAAGTGTGTAGTTACTGACATGAAAA  
ATTACATAGAGGCTGAACAGCAGATTGAGCAGGACAGAAAAATCAGCAGCTTGAAGATGGTACCTTGAGATT  
TTTCAGGCTAATGAAAAAAGATGAAGGAAAAATTAACAGCCTCAGAGACCCGTTGACCGCTCACACAAATCAA  
CATATGCATGATGAGAGTCCAGAGGAGAGGAGAGAAAGGTCAGAAAGATGGCCACAAGCTGATGAAAAACA  
GTAACCTACCCACTCAGGAAGCTCAGTGAATCCAATGAGGATGAATATCAGAGATCCACACTAGATATTTCT  
AATCAAGTGTCAATGACAAGAATCTTGAAGCAGCAGAGATGAGCACTTATCTTGTCAAGGATCTTTG  
ATCAGATTAAACAGCTCATTTCTCTCAAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGCAA  
AACCTTCAACTGTAATTATTGAGCTTTTGTGCTTGTAGTGGTCTGACCTCTTGTCTTCAAGGACAGTTTTC  
ATTTAATCCCTAATAACAAATAGTCAAGCTTCTTGAATGTAGGAGGCGCTGCTTGAAGCGGGCAGTGGC  
TTACACCTGTAAATCCAGCACTTTGGGAGGCCAGAGCGGTGGATCATTTGGGTCAGGCTGATCTCAAACTCT  
GAGTCTAGGTGATGCTTCCGCGCTCAGCCTCCAAAGTGTGATGTCAGCGGTGAGGACCTGCTGCTGCGGCA  
ATTTCTTTTAAAGCTGAATGATGGGGCCAGGACAGTGGTCAAGCTGTGATCCCAAGTAGCTTGGATTGTA  
AAGATGACACCACATGCTGGCTAATTTTGTATTTTGTAGTAGAGCGTGTAGCCAGGCTGTCTGATCTCTCT  
GACCTCAAGTGACCACTGCTCAGCCTCCAAAGTACTGGGATTACAGCGCTGAGGACCTGTGCTTGGCCTTGA  
GCATCTGTGATGTGCTTATGGCCATTGTATATCTTATCTCTTGGGGAATGCTGTCTCAAGTCTTTG  
CCTTTTTAAATTTTATTATTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT  
CAGTGGCAGCTCTTGGCTCACTGAGGCTCGACCTCTGGGCTGAGTGTCTCTCCACCTCAGCCTCCCTTGT  
AGTGTATTTTGTATTTTGTATTTTGTAGTGTAGTGTGTATTTTGTATTTTGTGGGAGACAGCATTTCAACATGA  
TGCCAGGCTGGTCTGAACCTCTGAGCTCAAGTGTCTGCTGCTTCAAGCTGCCAAAGTGTCTGGGATACAGA  
CATGAGCAGCTGACCTGGCAAACTCCCAAAATTAACACACACACAAAAAACCACTGATTCAAAATGGGCA  
GAGGGGCGGGGTGTGGCCCCAAGTACCAGGAGACTGAAGTGGGAGGATCGTTGGGATGAGAAGTCGAGGCTG  
CAGTGTGTCGAGGTTGTGCGACTGCATTCAGCCTGGACAACAGAGTGAGACCTGTCTC

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## **FIGURE 166**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVVFVSGLVINQVQLCTLALWPVSKQLYRRLNCRSLWSQLV
MLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGKK
YEADMCVRRPFLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN
FLSWATILLSPLFSFVLGVFASGSPLLILTLFLGFVGAASFVRRLLIGESLEPGRWRLQ
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 307-323, 335-352

**Tyrosine kinase phosphorylation sites:**

amino acids 160-168, 161-169



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## **FIGURE 167**

GATATTCTTTATTTTAAAGAACTGAAGTACT**ATG**CATCACTCCCTCCAATGTCCTGGGGCA  
GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTGCTTTAGCACTGGGGCACTTCTT  
GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCG  
GCTTACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG  
GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTT  
TTCTCTAACCTGGCATACCCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAA  
AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCCCTGGCCAGCTTCATTGT  
ACATGTGGTGTCTCTTGTGCTTCCTG**TAA**TGTGGTATGCCATGGGGTCTTGCACAAGCCT  
TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCTACTTAATATGTAGTC  
ATCCTGCAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT  
CTTGTTAATGCTCTCATAAGACCACTTGTTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTA  
TCTTTATGTGCGTTTGTGGTTGTATGGGTTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGC  
TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCCTACATGTGGTGGGTGCT  
CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCCCA  
GATGGTGTAGGGCCCAGCATTTGTAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA  
TGCAGTCTTGATTCAGTAGGCCAGGTTGGGCATCTCTAACAACTCCACGTTGATGCTGA  
TGCTGGTCTATGAACTATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC  
TCACACCTATGATCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT  
TCAAGACTAGCCTGGCCACATGGTGAACCCCATCTGTACTAAAAATACACAAATTAGCTG  
GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG  
AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAAGGGTGAC  
AGAGTGAGACTCTATGTCCAAAAAAAAAAAAA



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**FIGURE 169**

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCTCAGCCTCCCAAGGTGCTGTGA  
 TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCAC  
 AGGAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTAC  
 ATTAATACTGTTTTTTTGTTCTCTTGTAAGTACGCTTTACCTTCCTAACACAGAGGATCTGT  
 CACTGTGGCTCTGGCCCAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCAC  
 ACCGTCCTCCCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC  
 ACCAACTGTCTCAGTCTGGAGGCACTACTCGGGCAGTGCAAGTAGCTGAGCCTCTTGTA  
 GCTGCGGCTTCAAGGTGGGCTTGCCCTGGCCGTAGAAGGGATTGACAAGCCGAAGATTT  
 CATAGGCGATGGCTCCCACTGCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG  
 CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCAGCTGCCCGCCCAT  
 CTAACCTTTTCATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG  
 AACCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT  
 TATGTGACAGGACTTGCAATCTCTGGAACATGAGGGAACGCCGAGGAAAGCAAAGTGGCA  
 GGGAAAGAACTTGTGCCAAATTATGGGTGAGAAAGATGGAGGTGTTGGGTTATCACAAGGC  
 ATCGAGTCTCCTGCATTCACTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT  
 CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGATCCACGTACCAGCTGCTG  
 AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG  
 CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCTCCCTCCTTCCCTC  
 TGAGAGGCCCTCCTATGTCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG  
 GCTCAGTGTTGGCCAGGAGGTGAGCAAGGCCGTGAGAGCTGATCAGAAGGGCCTGCTGTGCG  
 AACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCT  
 CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT  
 TCAAATGATCTCCAAGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAA  
 TCCAAACCTAAGAACCCAGGTGATTAAAGATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG  
 CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTGAGGATTCAGGATTCAGACCCCTG  
 GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT  
 GTGTGCTGTATCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT  
 GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA  
 AAAAATAAAAAAGAATTATGGTTATTTGTAA

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**FIGURE 170**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277

&gt;&lt;subunit 1 of 1, 109 aa, 1 stop

&gt;&lt;MW: 11822, pI: 8.63, NX(S/T): 0

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA  
SPCWPLAGAVPSPPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD**Signal peptide:**

amino acids 1-15

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**FIGURE 171**

GCGGGCCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC  
 CCGCCGCCTCCTGCCCCGCGCC**ATGA**CCACCCAGCCGGTGCCCCGGCTCTCCGTGCCCCGCCGCGCT  
 GGCCCTGGGCTCAGCCGCACTGGGCGCCGCCCTTCGCCACTGGCCTCTTCTCTGGGGAGGCGGT  
 GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCCCTGTGG  
 CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC  
 CCTGGAGCAGCCGCAGGGGATTCTATGATGACCTGCGAGCAGGCCACAGCTCTTGGCCAACCC  
 TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC  
 CTGGCCCTGGCCCTGGCGCTGCCCCGCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA  
 GCCCCCGAGCTGGGACGGCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAAGATCGACCTCC  
 GGCTGAAGCCCGCCTTGGAGACCCTGGACGAGCTGCTGGCGGGCGGGCGAGGCCGGCACCTTC  
 GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCCTACTACGAGCGCTGCCTGCA  
 GCTGCTGCGACCCGGAGGCATCCTCGCCGTCTCAGAGTCTGTGGCGCGGGAAGGTGCTGC  
 AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG  
 GACGTCAGGGTCTACATCAGCCTCCTGCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT  
 C**TAG**GGCTGGCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC  
 CCTGAGTTTAAATTCGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 172**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQVPRLSVPAALALGSAALGAAFATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSR
MREHPALRSLRLLTLEQPQGDMMTCEQAQLLANLARLIQAKKALDLGFTFGYSALALAL
PADGRVVTCEVDAQPELGRPLWRQAEAEHKIDRLKPALETLDELLAAGEAGTFDVAVVDA
DKENC SAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRYIS
LLPLGDGLTLAFKI
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-25

#### **Transmembrane domains:**

amino acids 8-30, 109-130

#### **N-glycosylation site.**

amino acids 190-193

#### **Tyrosine kinase phosphorylation site.**

amino acids 238-246

#### **N-myristoylation sites.**

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

#### **Amidation sites.**

amino acids 31-34, 39-42

**FIGURE 173**

[illegible]

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## FIGURE 174

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMGYPHPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFFPD
KCKDKYKGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDERD
VMAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSE
EENSESSSESEKTSQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSDSDSVSKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV
DRISEWKRRDEARRRRELEARRRREQEELRRLREQEKEEKERRRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKSAKKPQSSSTEPARKPGQKEKRV
RPEEKQAKPVKVERTKRSEGFMSMRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAV
QKVNKAGMEKEKAEKLAGEEAGEEAPQEKAEDKPSTDLAPVNGEATSQKGESAEDEKEHE
EGRDSEEGPRCGSSEDLHDSVREGPDLDRPGSDRQERERARGDSEALDEES
```

### Signal peptide:

amino acids 1-13



**FIGURE 175**

GGGTTCCTCGTGGATTTACCTTTACCAACTCGAGATTGGGCATCATAGCCTCAATTAATTAATAAT  
 ACACACTTTGAAGAGAACAACTGTTTTCATCTAGTAAGTACTGTAAGAAGTCAATAAGCCGAAGGACAGA  
 TTTTCACCTTTTCTCTGCTTTGATGATGTCATAGCATGACCATGTGTTTCTTCAGTACGCTGGCACTTTGAAGCA  
 AATAATTTCCAGACTCAACTCAACCTACAAGACTGCTGCTTTCAAATAGCTGTATCTCCTTTTGGGTTCATC  
 AGAAGGAGCTGGATTTTCAAACCTCTCTCTTAGTAGAGGAAGAAGGACGAGCTGCTCTGGGAGCCAAAGACACAT  
 CTTTCTACTCACTGCTGGTGTACTTAAACAAAATTTAAGAAATTTATGGCCTCTCGAAGGAACGGGTGGGA  
 ATTATGTAATTAAGCTGGGAAGATGCCATACAGAATGTGCAAAATCTTCAGATGACTTTCAGCCCTATACACA  
 AACTCAATATATGCTGTGAAGTACGAGCATTCATCAAAATGTGGGTATATTGATCTTGGAGTCTACAGAAG  
 GGAATATTATTTCAAACCTAGACACACATAATTTGGAGTCTGGCAGACTGAANTGCTGTTCTCGATCCTCAGCGA  
 TTTTGGCTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTGGCAAGAATACGAT  
 CACTGATCCTCTGGGCTACTCATGACCACCACTCACTAGAACTGACATTTAGAGACACTTGGCTCAATG  
 AGCAAAATTTTGGAAACTTTTCTCATACAGACACACTACAATCCAGATGATGAATAATATTCTTCTTTCG  
 GAAATCACTTCAAGAGGACGACTCCGTAAGAACAACCTCTCTTTCAGTGTGGAAGAGTTTGTAAAGATGATG  
 AGAGGACAACGCGACCTGATAAACAGGTGGACACTTTTAAAGCCAGACTGATTTGCTCATCTCTGGAAG  
 TGATGGGCGACAGATACATTTTGTATGAGCTTCAGAAATTTATTATCTCCCCAAGAGAAGATAAAGAATACCTGT  
 AGTATATGGAGTCTTTTACTACAAAGCCCTCACTCTTCAAAGGGCTCTGCTGTTTGTGTATAGCATGGCTGACAT  
 CAGAGCGAAGTTTAAATGGTCCATATGCTCAATGAAGAAGTCAGACAACTCGTTGGGTGCGAGTATGGGAAGAAT  
 TCCCTATCCAGCGGCTGGTACATGCTCAAGCAAAAGCTAGCCCACTGATTAAGTCCACCAGGATTTTCCAGA  
 TGATGTCATCATGTTTCTAAAGCGGCACTCTGTGATGTATGCTGATACCCAGTTCCAGGAGGACCAACGT  
 CACAGAAATCAATGTGGATTACAGACTACACAGATAGTGTGGATCATGTCAATTCAGAAAGATGGCCAGTACGA  
 TGTAAATGTTTCTGGAACAGACATTTGAACTGTCTCTCAAAGTGTGCAGCAATTTCAAAGGAAGAAGTGAATATGGA  
 AGAGTGTAGTCTGGAGGAGTCGAGATATCAAGCACTCATCAATCTTGAACATGGAATGTCTCTGAAAGCA  
 GCACAAATGTCAATTTGGTTCCGAGATGGATAGTTCAGCTCTCTTGCATGACATGCGACACTATGGGAAGG  
 TTGGCAGCACTGTGTCTTCCGACAGAGCTCATGTGCGCTGGGATGGAATGCATGCTCGATATGCTCTTACC  
 TCTTAAAGAGGAGCTAGACGCGAAGATGAAATATGCGCACCACTACCCAGCTCTGGGACATCGAAGACAG  
 CATTAGTCATAAAGCTCTGATGAAGAAGTGATTTTGGCATGAAATTAACCTAACCTTTCTGGAATGTATAC  
 AATAATCCCAACAGCAAACTATAATAGTGATATCCAGAGTCCAGGGAGTGACATCCAGAGAGTTGAAGCCGCA  
 TGAAGAATCATCAAAAGGAATTTGGGTACTGTTCTGCAAGTTTCGAGAAGAAGTATCTGGGATATTATTCTG  
 CAAAGCCGAGGACAGACTTCATCCACACGCTGATGAAGCTGACTTTGGAATGTCTAGAAATGAACAGATGGA  
 AATAATCCGACAGGACAGACTGAGGAGAGGGCAGTGCAGAGTACTTTGGTGTAGTCACGGTTGAGATCAAGA  
 CTACATCAAAATCCTTAGACGCCAAATCTCAGCCTCAGCAGCACTTCGCGACAGATTCGCGACAGGAGGAAGCC  
 GACATCGAGAACAACAGGGGGGCCAAAGTGAAGACATCAGGAATTAAGAAGAAGCAAGAACTGAAGACATC  
 CAGAGACCTGGATGAGTCTGTTAGCTGTAGCCACCTAGTCTTTCATTAATTTAAAGAAGAAGATTTCTTACC  
 TATAAAACATTTGCCTTCTGTTGTATACCTTATAGTAATTCATAAATGTTCCCATGGAAGTTTGTCTAAGG  
 CACAGACAAATAATCTGCAATAAGACAATATGTGATGAATATAAGAAAGGCAAAAAATTCATTGCAACGATTTT  
 CCAAGAACAAATCTTGCAACGAAGAAATATAAGAAATTCCTAAAAATAGGGGGTTTACAGTTTGAATGTTT  
 TGTTTGTAGTTTGGAAATTTATGTCTATGAATAAGTTTGAGCTACAGCAAGCCCGGAATTTGTATGATGTATAAGG  
 GCTTTATCTCTCTCGGAATTTGCTATAGCATGGAATTTACATCGAGTTGTGCTATGTTCTTAGAACAGATATAT  
 CATTTCTTATGAGAAAGCAGCTACCTTTGGTAGGGAATAAGAGGTCAGACACAAATTAAGACAACTCCCATATT  
 AACAGGAACCTTTCTCAGTAGGCCATTCACTCTCGGAAGAGGTTAAGGAATTTGGAGAGGTGCATATTTCTCTTC  
 TGGGCACTGGGGTTAAATTTGATGTACTACAGAACTGATTTTACTGAAGGCAATGAATGTTTCCCCGAGGATTTCT  
 ATTGACTAGTCAGGAGTACAGGTTTACAGAGAGAGTTTGGTGCTTGGTATGTTTGTAGATATATACTAA  
 GCTCTACAGGACAGAAATGCTTTAATAATCTTTAATAGATATAGGAATAATTTAATAAAACAGGAAGAAC  
 TAATGATGTATAATGACTCTGTGAGGAAGCACTGATGAGGGATTTGTAGAAGACAGGAAGAAGACAGCCAT  
 AATTTCTGGCTTTGGGGAAGAACTCATATCCCATGAAGAAGGAACAAATCAAAATTAAGGTGAGAGTAAATGTAT  
 TGGAGCTCTTTTCACTAGGATATAGTATAGCTGCGCAATTTGTAATTCATCTGTAAAAAAATTCAGATATAACA  
 AACTGCTAGCAAAATCTGAGGAACACATAATTTCTTGAAGAATCATAGGAAGATGACATCTTTATTTATAAC  
 AATGATATTCAGTATATATTTTCTCTCTTTAAAAAATTTATCATGCTGTATATTATTTCTTTTACTGCT  
 CTTTATTTCTCTCTGTATATGGAATTTTGTGATATATTTGTGTAATAGGAAGAACAAATATATACACACAGA  
 GAAATTAAGAAATGACATTTCTGGGAGTGGGATATATTTGTGTAATACAGAACAGGTGATAAATTTTAAAC  
 ACGGAAAGGGGTAAATTAACCTTTGCATCTTCACTCAACCTTTTCTCATTTGCTGAGTTAATCTGTTGTAAT  
 TGATATGTTGTTTGTAAATTTAAGCAATAAATAGGCTGCTACATGT

## FIGURE 176

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
<subunit 1 of 1, 777 aa, 1 stop
<MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTyKDLLLSNSCIPFL
GSSEGLDFQTLTLLDEERGLLLGAKDHI FLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGR LKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDHHYIRTDISEHYWLN GAKFIGTFF
IPDTYNPDDDKIYFFFRESSQEGSTSDKTIILSRVGRVCKNDVGGQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPD DVISFIKRHSVMYKSVYPV
AGGPTFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVV SISKEKWNMEEVLEE
LQIFKHSSII LNMELSLKQQQLYIGSRDGLVQLSLHRCDTY GKACADCLARDPYCAWDGNA
CSRYAPTSKRARRRQDVKYGDPITQCWDIEDSISHETADEKVI FGFIEFNSTFLECIPKSQQA
TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMY YCKAQEHTFIHTIVKLTLN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKRNRHRDLDELPRAVAT
```

### Important features of the protein:

#### Signal peptide:

amino acids 1-36

#### N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

#### Tyrosine kinase phosphorylation site.

amino acids 571-576

#### Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

**FIGURE 177**

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGAGAGGTCATCCTGGAGCATGCCACC GCGGGAGCAGA  
CAACCTCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTCTCTCAGGAGCCTGGTGTAATTTTCCCCACCCAC  
CTCAGCAGTTTCAGCCAGCAGGGGACTGATCAGGTGTGTCTCCTGGAGTGGGGAGCAGAAGGCGTGCGTGGCAAGA  
GTGGCCTGGAGAAAGAGGTTGACGCGTTGACCAGCCGAGCTGCCCGTGACTACAAGATCCAGAACATGGGCATC  
GGGTGAGGTGGGGGGGACAGGTGTCTGTGCACCTTCTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTTGG  
AGCCATTGAGGGTGTCATGGAGCTACAGAGGGGAGGGAAGGTATTTAAAGTTAACAGTGTGGCACAAATAGTTAA  
GAGCACAGTTTTTGGAGCTAGACCACATAGGTTCAAATTTCTCTTCTGTGCTTCTTAGTTCTGTAGCCCAAGGT  
AAGGGAGTGACTTAACCTCTCTGGACTCAATTTCTCATCACTAAAGTAGGGCCAAATAAGCACCCACTCAT  
AGGGAAGATTAAATGACATAATGTATGTGATGCACTAGCAAACTAGCAAACTACCACTGCCATAGTCAATGCCACAG  
TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACCAGGTACTGCAACGACTGGAGCAGAGGGCGAGCAGGCTT  
CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGCATCCGCGGGGACAGGTTAGGCC  
AGGTGAAGGGGGCTGCCCGCTGCCCTGTCTGACAGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA  
TGACCCAGGGCCAGGATGAGGTGGAGCAGGAGCGGGGCTCAGTGAGGCTCGGCTGTCCAGAGGGACCTCTCTC  
CAACCGCTGAGGATGCTGAGCTTTTGTACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCTGCC  
CCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACGTGGTATTTTCGTATCAGGCAGGGCGTGAGGATG  
AGCTGACAATCAGGAGGGTGAGTGGCTGAGGAGTCATAGAGGAGGAGATGCTGACGAATGGGTCAAGGCTCGGA  
ACCAGCAGCGCGAGGTAGGCTTTTGCCCTGAGCGATATCTCAATTTCCCGACCTCTCCCTCCACAGAGCAGCA  
AAGACAGTGACAATCCCTGCGGGGACAGAGCCACAGCATTTCTGGCACAGGCCCTGTACAGCTACACGGACAGA  
GTGCGAGGAGGAGCTTCTCTTCCCTGAGGGCACTCATCCGCTGCTGCTCGCGGGCCCAAGATGAGATGATGACG  
GCTTTCTGGAGGGGAGAAATTTGGGGGCGGTGTGGGGTCTTCCCTCCCTGCTGGTGGAGAGCTCTTGGCGCCCC  
CAGGGCCACTGAACCTCTGTGACCTTGAACAGATGCTGCCCTCTCTCTCTCCCTCTCTCCCACTGCAC  
CTACTCTCTGTGTTGGATGGGCCCCCTGCACCTGTCCCTGCTGGGACAAAGCCCTGGACTTCCCTGGGTCTCTGG  
ACATGTATGGCACTCTGACTCAGGCCAGCTGCGTCCACCACTCCCGCGGGTAAAGCCCGGATCTGTGCCACC  
CAGATCCCTCACTGAGAGCCAGGAGGCTTGACCCCACTGATGCTGCTCTCCCTATCTCAAGCTCTGCAGA  
CCACCACTCAATGCTCAGAGACACACAGCAAAAGCTGGAATCGCCCTTATTTCCACCTCCCAAGGGT  
GGAACTTGCCCTTCCATTTCTAGAGCTGGAACCCACTCTTTTTTCCCATTTGTTCTATCATCTCTAGGAC  
GGAACACTACTACTTCTCTTCTGTGACCTATCTAGGCTGGTGAATGAACTCTCTGGGGCTGCCAACCC  
ATCCATCAAGGTCTCTAGTAGTTCTGGCCCACTCTTTCCCACTCCGTCATGACCAACCCCACTCTGAGAT  
CCAGGCTCACTGGGGTTGGGCTGGGGAGAGGAACAGGCTTGGGAATCAGGAGCTGGAGCCAGATGCGAAGCAG  
CTGTATGTCTGAGCGGATTTATGACAATGAATAAAGGGCAGGAAGGCCAGGCAGGGCTGGGCTCTTTGTG  
CTAAGAGGGGCAGGGGCTCTCAGGGCCCTTATGCTTTAGGGGCCACCAAGCGCAGGGGCTGCTGCCACTGCCAC  
GCTCTATCATATGAGAGCAGGTTTGGGGAAAGCGGGGACAGCAGCTTGTGACGAGGGGAGGAGAGAGAC  
TGAGGGGCTGTGACTCTCTGAGGCCCCAGCTGAGACTGTGCAACTCCAGGTGGAATGAGAGCTGTGTCAC  
AGCTGGGGGGAGCTGTGCTGAGTGAGGGGAGGGCTTTACGCCCAACCAACCCCTGGCCCTGCAGCTGTGGTAG  
TCATCAGCAATGAGGAGACTTGGAGAGAGGAAGAATAACACTGTGCTTCTGTCTCAAGCTGTGTCAGC  
TTTTCCCTGGGGCTCAGAGACCTTCCCTACTCCACCACAAACCAAGGGATTTATAGCAAGGCTTAAGCGCTC  
AGTTTACTCTGGGGTCTCAGGAGGCCAAAGGCTTAATAAGTTTAAGTAGGTATGGGAAGATGAGATTAACCTGA  
TTTAGGGCTCAGGCAGACTCACTCATACCTCTCCCTGCTGGTGTAGAGACACTGAGAGAAGGGGAGGGG  
TCAACAATGAGAGAGCAGAGTAGTCTATCATGCTGCCCCAGAGTAGAGACAAAGAGCCAGCCAGCTGAC  
AGTCCGGGCTGTGTTTTCTTACTGCTGATCAGAAAGTGTCTGGTTTGTCTGAGCTGCCATTTGGCTCTTGAAGTG  
CGAGCCCTGGGCTTGGGCCCTCTCAGGGCAGCATCCCTGCTTGGGCTCGGCTCGCCAGACCTGACCAACCCCTGC  
CAGGAGGGGTAGGCTGCTCTGCTGAGTCTCTCATCTCTACTGGGGGCTGGCTAGGACCTGGGGCTGTGGC  
TCTCAGGGGAGGCTCTCAGGGCAGCATCCCTGCTTGGGCTGCTCCGAGACCTGACCAACCCCTGC  
GGTCTGTGCCCCACAGAGCCCACTGCTGTGTGGGGAGCCATACAGCTGTGCTGCACTCATAGCGCT  
TCTCAATGTGTGTACCCGGAAGCTGGAGGGGAGGAACACTGGGTTTAGAGCACAACTCAGAGGCTCTGTG  
GGCTCCCTCTCAGCAGGGACATCTGASITTTGGTGGCTACTTCCCTCTGGCTAAGGTAGGGGAGGCTCTC  
AGATTGTGGGACATCTGTAGCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAGAGCCCAAGCCCACTT  
TTGGGATGAGTGCTGATCAGTGGGCCCCCTACCTCAGCCCCCTTCTCTGGAGCACTTGCCCCACTGCCCCA  
CAGAGAGACAGTGGTCTCCCTGTCCGGGGGCGGCTTTTCTCTCTGGAGCGTCCCTGACGCAAGTGGAG  
GGCTCTTGTCTGGCTGCAATGGATGCCAAGGGGCTGCAGAGCCAGGTCAGCTGTGTGATGATGAGGAGGGGCT  
CGTCTTGGAGGCTGGAGGTGCATCCCACTGGACAGCAGGAGGAGGGAGTGAGGGTAACATTTCAATTTCTCT  
TCATGTTTGTCTTACGTTCTTTGAGCATGCTCTTAAACCCCAAGAGGCGCAATTTCCCCAGGCCCACTTT  
TTCTTGTCTTATCTAATAACCTCAATATTAAG

**FIGURE 178**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401

><subunit 1 of 1, 370 aa, 1 stop

><MW: 40685, pI: 4.53, NX(S/T): 0

MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA  
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS  
DFEECEETGELFEEPAPQALATRALPCPAHVVFQAGREDELTITEGEWLEVIEEGDADEW  
VKARNQHGEVGFVPERYLNFPDLSPSSQSDSNPCGAEPATAFLAQALYSYTGQSAEELSFP  
EGALIRLLPRAQDGVDDGFWRGEGGRVGVFPSLLVEELLGPPGPPELSDPEQMLPSPSPPS  
FSPAPPTSVLDGPPAPVLPFGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHDPDLT

**FIGURE 179A**

CAAGCGGAGACCCACAGACCATATGCACGAGAGAGACAGAGGAGGAAGACAGACGACAAGGCCACAGCGGCAAG  
GAGGCAAGGACAGCGGACGACGACAGCGGCCGACGAGCTCAGAGTCTCTACAGAGGAGAGCCAGGACAGMCTCGA  
AGACAGCGGACGGGAGAGACCAAGATCCAGGAAGAAGGGGCTCAGGAGAGAGATTTGGAGAACCCAGACCTCCG  
GCACCTCTCCCAAGCCCAAGSACTAAGTTTTCCTTTTCTTAAACGGTCTCAGCCCTCTTGAAATCTTTGGC  
TCTGACCTTTGCAGAGAGTCCAAGCCCCAGGCTACAGAGAGAGAGCTTCCAAGTCTAGGGTGTGGAGGACTTGGT  
GCCCTAGACGCGCTCAGTCCCTCCAGCTCAGTACCGAGTGCATCTCCAGACAGAGCTGCATCCCGGAGGGGG  
TCTGGCAGGGCGCTGGCTTTGGGAGCCCAACCTGCTCTGCTCCCATTTGTCCGCTCTCTGGCTTGGTGTG  
GCTGCTTCTGCTACTGCTGGCTCTCTCTCTCCCTCAGCCGCTGGCCAGAGCCCCCTCCCGGGAGGAGGATAT  
CGTTGTTTCCAGAAAGCTCAACGGCAGCGTCTGCTGCTGCTGGGGCGCTTCCAGGCTGTGTGGCTGCTGCA  
GGCTTTTGGGAGAGCTGCTACTAGAGCTGGAGAGAGTCCGGTGTGCAGTGCAGGGGCTGCAGATCGAGT  
CTGGGCGACGGCGCTGAGCTGCTGGGTGGAGCAGACTGGCACTACTGACTGCGACCATTAAGTGAAGATC  
GGAGTCGGTGGCATCTTGCTCAGTGGGATGGGGAGCGCTTTAGGCGTGTACAAATTCGGGGGCGTAAGTCCA  
CTTCAGCCCTCGAGGGGAGAGCCCTAACTCTGCTGGGGAGCTGGGGCTCATCTCTACCGCGAAGAGTCC  
TGGCCGCGGTCAAGGTCAGATGCAACTGCAAGCTCAAGCTCCTCTGGAAGCCCCAGCCCAAGCCGGAAGACAA  
GGCCTTTGCTTCACTAGTTAGATTTTGGAGACACTGGTGGTGAGATGACAAGTGGCGCATATCCAGGCTGG  
GGGCTTAAAGCGCTACTCTCAACAGTAGTGGCAGCAGCCAGAGGCTCTCAAGCACCAGGATTCGCAATCC  
TGTGACCTTTGGTGTGACTCGGCTAGTGATCTGGGGTCAGGCGAGGAGGGGCCCAAGTGGGGCGGCTGCGC  
CCAGACCTTCGCGACAGTCTGTGCTCGGCACGAGCTGCTCAACACCTGAGGACTGGGGCTCAGACATTTGA  
CAGACCAATTTCTTTTACCCTGGACGCTGGTGAGTCTTCACTTTGCGACAGCTGGGTATGGCTATGTGG  
CACCGTCTGTGACCCGGCTCGAGGCTGTGCCATTTGGAGAGTAGTGGGCTCCAGTACAGCTCTGCTGCTCA  
TGAATGGGTATGCTTCAACATGCTTCACTGACAACTCAAGCCATGATCATGTTGAATGGGCTTTGAGAC  
CTCTGCGCATCTCATGCGCCCTGTGATGGTCTATGTGATCTCGAGGACCGTGGTCCCCCTGAGTCTGCCGCTT  
CATCATGACTTCTTGCAATAGGCTATGGGCACTGTCTTTAGACAACCAAGGCTCATTTGATCTTGCTGT  
GACTTTCTCCGGCAAGCAATGATGTCTGACCGCAGTGCAGCTGACCTCTCGGGCCGACTCAGGCAAGTGTCC  
AGACTTCGCGCGCGCTGTGTGTGCGCTCTGGGCTCTGGGCACCTCAATGGCCATGCCATGCCAGACAAACA  
CTCGCCCTGGGCGGATGGACACACTCGCGGGCCGACAGCGCTCGATGGGTGTGCTGCTGCTCCATGTAGGACA  
GCTCGAGCAATTCAAATTTACACAGGCTGGTGCTGGGGTCTTGGGACCATGGGTGACTGCTCTCGAGCTG  
TGGGGGGTGTGTCCAGTTCTCTCTCGAGACTGCGACGAGGCTGCCCCCGCAAGTTGGGCAAGTACTGTGAGG  
CGCGCTACCCGCTTCGCTCTCTGACACATGAGACTTGCCCACTGGCTCAAGCTGACCTTCGCGAGGAGG  
GTGTGCTGCTTCAACACCCGACCGACCTCTTCAAGAGCTTCCCGAGGCCCATGGATGGGTTCTCTGCTCTAC  
AGGCTGGCCGCCCGAGCAGCAATGCAAACTCACTCGACGGCCGGCCTGGGCTACTATGCTGTGCTGGAGC  
ACGGTGTGTAGTGGGACCCCTGTCCCCGAGACGCTCTCGGCTCTGTCTCAGGCGCGACTCATCATCTGCTG  
CTGTATGCTCATTTGGCTCCAAGAGAGTTTGACAACTGATGCTGGCGAGGGGACGTTTGGTGTGAG  
CAAGCACTCAGGCTCTTCAAGAAATTCAGTACGGATACAAATATTTGGTCACTATCCCCCGGGGCGCCCA  
CATTTTGTTCGGCAGAGGAAATCTGGCCACGGAGCATCTACTTGGCCCTCAGCTTGGCATGGCTCTGCTCA  
TGCCCTTAATGGTAGATACAGCTGATGCCCTCCCAACATTTGGTACTGCTGGGACAGTCAGCTTTGCGCTA  
CGGCGGGGCACTCGACCTACAGACACTCTCAGGCGCACTGGGCACTGGCCAGCCTTTGACACTGAAGTCT  
AGTGGCTGCAACCCCGACAGCACCGCTCCGATCTCTTCTGTGCCCGGCGAGCCCTTCAACGCCAC  
CCCCACTCCCGAGCACTGCTGACCCAAAGACAGAGTTTGGAGATCTTCGGCGGCGCCCTGGGCGGGCAG  
GAAATTAACCACTCATCTCCGGCTGCCCTTTCTGGCGACCGGGCGCTCGCATTTAGCTGGGAGAAAGAGAGACT  
CTGTTGTGCTCATCTGCTAAGACTCATGGGAGGGAGGCTGTGGGCTGAGACCTGCCCTCTCTCTGCCCTAAT  
GCGGAGCTGGCCCTGCCCTGCTTCTTCTGCCCTGGGAGCAGTATGGTGTATGTAAGGGGCTGACAGAC  
AGCCCTCATCTAAATCGCCCCCTGCTCTCGCTCGGGTCAAGAGGAGGGGGAGCAGGAGGGGCTCGGGCC  
CAGTTGTATTTTATTAGTATTTATTCACTTTTATAGCACAGGAAGGGGACAAGGATAGGCTCTGGGAA  
CTGACGCTCGACCCCTCATAGGCTCATGCCCTGCGGGGTAGGAATACAGGGTGGTGGTGAATAGTTATGTG  
TGTATGCGTGTGTGTGTGTGTGAAATATGTGTGTGCTATGATGTAGGTACAACTGTTCTGCTTTCTCT  
TTTTTTGATTTTATTTTGGGAAAGAAAGTTCAAGGTAGGGTGGGCTCTCAGGAGTAGGAGGATCTCTTT  
TTTTTTTCTTCTTCTTCTTTTTTTTTTGTGTGAGCAAGATCTGCCTCTGTGCCCCAGCTGGAGTGAAT  
GCAACATCTCGGCTCATGCTATCTCGCCTCCGGGTTCAAGTATTTCACTCGCTCAGCTCTGAGTGTGCT  
GGATTAGGCTCTGCCACAGCCGACGCTAATTTTTTGTGTGTTTGGAGACAGAGTCTGCTATTTGTG  
ACAGGGCTGGAAATGATTTGAGCTCATGCACTGCAACTTGGCCACTGGGTTCAGCAATTTCTCTGCTCAGCTCT  
CAGTAGTCACTGATATAGGCACTACCAACGCGCCGCTAATTTTTGATTTTATGAGAGCGGGGTTTAC  
CATGTTGGCAGCGTGTCTGCAACTCTGCACTTAGTGAATCACTGCGCTCATCTCCCAAGTCTCGGGAT  
ACAGCGCTGAGCCACGCTGCTGCCACCGCCAACTAATTTGTATTTTATGAGACAGGGTTTCAACATGT  
TGGCAGGCTGCTCTGAACTCTGCACTCAGTATGCACTGCTCGCTGGCCCTCCAAAGTCTCGGGATACAG  
TGTGAGCACACGCGCCGCTACATTTTTTAAATGAATTTACTAATTTATGTGATCTTTTGGATGACAGAC



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**FIGURE 180**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

&gt;&lt;subunit 1 of 1, 837 aa, 1 stop

&gt;&lt;MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPRGLAGRWLWGAQPCLLLPVPLSWLVWLLLLLLASLLPSARLASPLFREEEIV  
 FPEKNGSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEP  
 GTYLTGTINGDPESVASLHWDGALLGVLYRGAEHLQLPEGGTPNSAGGPGAHLRRKSP  
 ASGQGPMCNVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYYLLTVMAA  
 AAKAFKHPSIRNPVSLVTVRLVILGSGEEGPQVGPSAAQTLRSFCAWQRLNTPEDSGPDHF  
 DTAIFLTRQDLCGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAAHELGHVFNMLHD  
 NSKPCISLNGPLSTSRHVMAFVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL  
 PVTFFPGKDYDADRQCQLTFGPDSRHCPQLPPFCAALWCSGHLNGHAMCQTKHSPWADGTPCG  
 PAQACMGGRCCLHMDQLQDENIPQAGGWGPWGPWGDSCRTCGGGVQFSSRDCTRPVPRNGGKY  
 CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRDLEFKSFPGPMDWVPRYTGVPQDQCK  
 LTCQARALGYYYVLEPRVVDGTPCSPDSSSVQVQGRCIHAGCDRIIGSKKKFKDKMVCVGGDG  
 SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQGNPGHRSIYLALKLPDGSYALNGEYTL  
 MPSPTDVVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT  
 ESTPRPTPDWLHRRQAILEILRRRPWAGRK

**Important features of the protein:****Signal peptide:**

amino acids 1-48

**N-glycosylation site.**

amino acids 68-71

**Glycosaminoglycan attachment site**

amino acids 188-191, 772-775

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 182-185

**Tyrosine kinase phosphorylation site.**

amino acids 730-736

**N-myristoylation sites.**

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-  
 172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-  
 582, 679-684, 682-687, 763-768

**Amidation sites.**

amino acids 560-563, 834-837

**Leucine zipper pattern.**

amino acids 17-38, 24-45

**Neutral zinc metalloproteinases, zinc-binding region signature.**

amino acids 358-367

**FIGURE 181**

CAGCAGTGGTCTCTCAGTCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**  
CAAAGAATCCTCCAGAGAATTGTGAAGACTGTACATTCTAAATGCAGAAGCTTTTAAATCC  
AAGAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCT  
AATTGTCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA  
TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTACATGGAAATTGATCCTGTG  
ACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT  
TAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA  
TTAAAGTGATTCCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC  
ACAACCTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA  
TTTTCTTAAAAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC  
CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT  
CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT  
AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAAGTCCCAATAAATGACTATACATG  
AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGATTTACTGCCGT  
CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA  
CTGCTACCAAGGAGGACGAGTCATCTGTGTCATCATGCCTTGTAAGTGGTGGGTGGCCC  
GCATGCTGGGGAGGGTCT**TAA**TAGGAGGTTTGAGCTCAAATGCTTAACTGCTGGCAACATAT  
AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT  
CTCCAGAATTACTGTAGGTAATTCCTCTCTCATGTTCTAATAAACTTCTACATTATCACC  
AAAAAAAAAAAAAAAAAAAA



## **FIGURE 182**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFKSKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPPKAY
DMEHTFYSNGEKKKIYMEIDPVT RTEIFRSGNGTDETLVHDFKNGYTGIFYVGLQKCFIKT
QIKVIPFSEPEEEIDENEEITTTFFEQSVI WVPAEKPIENRDFLKN SKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGEIFDPM LDERGYCCICYCRGRNRYCRRVCEPLLGYPYPYCYQGGRVICRVIMPCNWWV
ARMLGRV
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-40

#### **Transmembrane domain:**

amino acids 25-47 (type II)

#### **N-glycosylation sites.**

amino acids 94-97, 180-183

#### **Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

#### **N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

#### **Microbodies C-terminal targeting signal.**

amino acids 315-317

#### **Cytochrome c family heme-binding site signature.**

amino acids 9-14

# **FIGURE 183**

GCGGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCAGGGAGCTGCC  
 CGGCTGGCCTAGGCAGGCAGCCGACCA**ATG**GCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT  
 GCTCAGCTTCTGGGCATGGTGGGCACGTTGATCACACCATCCTGCCGCACTGGCGGAGGA  
 CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAG  
 TGTGTGTGGCACAGCACAGGCATCTACCACTGCCAGATCTACCGATCCCTGCTGGCGCTGCC  
 CCAAGACCTCCAGGCTGCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT  
 GCGCCTGCGCCGTCATCGGGATGAAGTGACACGCGCTGCGCCAAGGGCACCCGCCAAGACC  
 ACCTTTGCCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT  
 CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA  
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT  
 GGCACCCCTGCTTTGCCCTGTCTGTCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCGGCC  
 CAGGGCCACCACGACCACTGCAAAACACCGCACCTGCCTACCAAGCCACAGCTGCCTACAAAG  
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG  
**TGA**GTCCCCACAGCCTGCTTCTCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC  
 AATGGAGGCAGGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATA  
 ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA  
 AGCTCTCTATACCAAGACTGAAAAAAAATCCTGTCTGTTTTGTATTTATTATATATAT  
 TTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT  
 TGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTTATGAAAAAAAAAAAAA

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# **FIGURE 184**

MASTAVQLLGFLLSFLGMVGTLLITLPHWRRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY  
 QCQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAGTTPAKTTFAILGGTL  
 FILAGLLCMVAVSWTTNDVVQNFYNPLLPSPGMKFEIGQALYLGFISSSLIGGTLLCLSCQ  
 DEAPYRPFYQAPPRATTTTANTAPAYQPFAAYKDNRAPSVTSATHSGYRLNDYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-103, 115-141, 160-182

**FIGURE 185**

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG  
 CAGGCGGCAGGGCGGGCGGCCAGGATC**ATG**TCCACCACCACATGCCAAGTGGTGGCGTTCTCT  
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC  
 AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC  
 GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTCACCATCTGGGACTTCCAGC  
 CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCTGGGTGCCATTGGCCTCC  
 TGGTATCCATCTTTGCCCTGAAATGCATCCGATTGGCAGCATGGAGGACTCTGCCAAAGCC  
 AACATGACACTGACCTCCGGGATCATGTTCTATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT  
 GTCTGTGTTTGCCAAATGCTGGTGACTAACTTCTGGATGTCACAGCTAACATGTACACCG  
 GATGGGTGGGATGGTGCAGACTGTTCAGACCAGGTACACATTTGGTGCGGCTCTGTTCTGTG  
 GGCTGGGTGCTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG  
 CCTGGCACCAAGAAACCACTACAAAGCCGTTTCTTATCATCGCTCAGGCCACAGTGTTG  
 CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAAACCCAAACCAAGAAAG  
 ATATACGATGGAGGTGCCCGCACAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA  
 TGTG**TAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAA  
 AACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGC  
 CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC  
 ACCATAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT  
 TTCTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCAC  
 ATTTTGATGATTAGACAGACTCCCCCTCTTCTCTCTAGTCAATAAACCCATTGATGATCTA  
 TTTCACAGCTTATCCCCAAGAAAACCTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTT  
 CTGCTGTTTGAATTTGTCTCCCCACCCCAACTTTGGCTAGTAATAAACACTTACTGAAGAA  
 GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG  
 TGATCTTAAAGTTACCAAAACCAAGTCATTTTCAGTTTGAGGCAACCAACCTTTCTTACTG  
 CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAG  
 TCCTCTTTCTGTGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAAATTATTTTTTTTAAT  
 TTAAGTCCTAAATATAGTTAAATAAATAATGTTTGTAGTAAATGATACACTATCTCTGTGA  
 AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTTGACATTGTCT  
 ATATGGTACTTTGTAAGTCATGCTTAAGTACAAATTCATGAAAAGCTCACACCTGTAATC  
 CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGTTCGAGACTAGCCTG  
 GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG  
 GCATACACCTGTAGTCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGG  
 AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA  
 TCTGTCTAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAA  
 ACTAATTTCTTAA



## FIGURE 187

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCGG  
GAGTCCAGCTGGCTAAACTCATCCAGAGGATAATGGAACCCCATGCCTTAGAAATCGCTG  
GGCTGTTTCTTGGTGGTGTGGAAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGG  
AGAGTGTGGCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACCTCTGGGAAGGACTGTG  
GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG  
CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTCCGTGATGTCCTTC  
TTGGCTTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAA  
GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC  
TCATCCCTGTGAGCTGGGTGGCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT  
GTTGCCCAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGCT  
GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACA  
GATACTCGATACCTTCCCATCGCACAAACCAAAAAAGTTATCACACCGGAAAGATCACCG  
AGCGTCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTAACTTTACTATAAAGC  
CATGCAAATGACAAAAATCTATATTACTTTCTCAAATGGACCCAAAGAAACCTTGATTTA  
CTGTCTTAACTGCCTAATCTTAATTACAGGAACGTGCATCAGCTATTTATGATTCTATAA  
GCTATTTACAGCAGAATGAGATATTAACCCAAATGCTTTGATTGTTCTAGAAAGTATAGTAAT  
TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTTATCATTTACTTCAAATGACATTGCT  
AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG  
TGTAACATTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG  
TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAATCATGGATAGGGTTG  
AAGAAGGTTACTATTAATTGTTTTAAAAACAGCTTAGGGATTAATGTCTCCATTTATAATGA  
AGATTAAAAAGAGGCTTTAATCAGCATTGTAAGGAAATGAATGGCTTTCTGATATGCTG  
TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTCTCCAGAGGCTTTTTTT  
TTCTGTGTATTAAATTAACATTTTTTAAACGCAGATATTTGTCAACGGGCTTGCATTCA  
AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG  
GTTTTAGGAAAGTGAAATATTTTTGTTTTGTATTTGAAGAAGATGATGCATTTTGACAA  
GAAATCATATATGTATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC  
AATATAAATAAAGAGCAGAAAAATATGTCTTGGTTTTTCATTGCTTACCAAAAAACAACA  
ACAAAAAAGTTGTCTTTGAGAACCTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATG  
TCATTTTTGTTCTGTGAAAAATAAATTTCTCTTGTACATTCTGTGTAGTTTTACTAAA  
ATCTGTAATACTGTATTTTTCTGTTTATTTCAAATTTGATGAACTGACAAATCCAATTTGA  
AAGTTGTGTGCGACGCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTTTATACATTTATA  
TTAATAAATGTACATTTTCTAATT

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**FIGURE 188**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

&gt;&lt;subunit 1 of 1, 225 aa, 1 stop

&gt;&lt;MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM  
QCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI  
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGALFCCVF  
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

**FIGURE 189**

TCGCC**AT**GGCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCTGACACTGCTGGGCTGGGTG  
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT  
CGTGGTGGCCAGGTGGTGTGGGAGGGCCTGTGGATGTCTGCGTGGTGCAGAGCACCGGCC  
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT  
GCCCTCTGTGCATCGCCCTCCTTGTGGCCCTGTTGGCTTGTCTGGTCTACCTTGTCTGGGGC  
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGTCACTCTGGGA  
TTGTCTTTGTCTCTCAGGGGTCTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC  
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAAGCGGGAGCTGGGGGCCTCCCT  
CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGTGGTGGGGGTGCTGTGCTGCACTT  
GCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCC  
GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGCT**CTG**ACGTGGAGGGGAATG  
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGT  
CGTACCTTTTGTTTCTGCCTCCTGCTATTTTTCTTTTGGACTGAGGATATTTAAATTCATTT  
GAAAACTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCTTGG  
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC  
CAGTCAAGCTATGGAATAATGCGGAGGCTGCTTGTGTGCTGGCTTTGCAACAAGACAGAC  
TGTCCCCAAGAGTTCCTGCTGTGCTGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG  
CCCCCATCTACTCAGGTCTCTGGAGCTCCTCTCTTACCCCTGGAAAAACAATCATCTG  
TTAACAAAGGACTGCCACCTCCGGAACCTTCTGACCTCTGTTTCCTCCGTCTGATAAGACG  
TCCACCCCCAGGGCCAGGTCCGAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC  
CTTCTGCCCTGCCCCCCCTGCTCTACCCCTTTTACTCACAATTTTATCAAATAAAGCATG  
TTTTGTAGTGCA



**FIGURE 190**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736

><subunit 1 of 1, 220 aa, 1 stop

><MW: 23292, pI: 8.43, NX(S/T): 0

MASAGMQILGVVLTLLGWVNLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM  
QCKVYDSSLALPQDLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV  
FVISGVLTLIPVCWTAHAIIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLGGGLLCCTCP  
SGGSQGPHSHMARYSTSAPAIISRGPSSEYPTKNYV

**Transmembrane domains:**

amino acids 8-30 (type II), 82-102, 121-140, 166-186

**FIGURE 191**

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAAGGCTTCCACGTTCTACATCTTG  
 AGCATCTTCTACCACTCCGAATTGAACCAGTCTTCAAAGTAAAGGCAATGGCATTATTTATCCC  
 TTGCAAATTGCTGGGCTGGTTCTTGGGTTCTTGGCATGGTGGGGACTCTTGCCACAACCCCT  
 TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC  
 TGGGAAGGGCTCTGGATGAAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA  
 TAGCTCCTTGTGGCTCTCCCGCTGCCCTGGAAACAGCCCGGGCCCTCATGTGTGTGGCTG  
 TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA  
 GGCTCTAACGAGAGGGCCAAAGCATACCTTCTGGGAACCTCAGGAGTCCCTTCATCCTGAC  
 GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA  
 ACCCAGCCATCCACATAGGTGAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA  
 AGCGCTGCTGTCTCTTCATTGGAGGGGCTCTGCTTTGTGGATTTTGTGTGCTGCAACAGAAA  
 GAAGCAAGGGTACAGATATCCAGTGCCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA  
 ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGCTTAATGCCTCCTTTTGGCTCCAAGT  
 ATGGACTATGGTCAATGTTTTTTATAAAGTCTGCTAGAAACTGTAAGTATGTGAGGCAGGA  
 GAAC TTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG  
 AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAATGCATTGACTATTGTTG  
 GACCAATCGCTGCTCCAATTTTCATATTCTAAATTCAGTATACCCATAATCATTAGCAAG  
 TGTACAATGATGGACTACTTATTACTTTTGGACCATCATGTATTATCTGATAAGAATCTAA  
 GTTGAAATTGATATTCTATAACAATAAACATATACCTATTCTA

## **FIGURE 192**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737

><subunit 1 of 1, 173 aa, 1 stop .

><MW: 18938, pI: 9.99, NX(S/T): 1

MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER  
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDFYNPAIHIGQKRELGAALFLGWASAAVL  
FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV

**Important features of the protein:**

**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

**N-glycosylation site.**

amino acids 161-164

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# **FIGURE 193**

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAGATCACTGGGGGT  
 CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC  
 AAAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA  
 CATACTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACCTTGTGTACC  
 GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTTAAATTCTCCA  
 TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG  
 AGTTTCTTTCAGTTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTGAGAGTAATCTTG  
 ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT  
 TTTTTTTTTAACACGTCAATAAAAAAATAATCTCCAGA

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# **FIGURE 194**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLLCTVVYFCSSEASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN  
ECHLCTESLKSNGRVQFLHDGSC

**Signal peptide:**

amino acids 1-19

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## **FIGURE 195**

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC  
CGCCGCCATGGGCTGCCTCCCCCGCGCGGCTGCTGTCTCTGGCCCTGACCGGGCTGGCGCTGC  
TCCTGCTCCTGTGCTGGGGCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATGCTTCAA  
AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA  
ATTCTTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGC  
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC  
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA  
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCG  
TCAACTACGATGACTACTTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATT  
TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTACGAGAT  
CTTTTCTACCTACTTTGTGTGATCAAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTTT  
TGATATTTTCATGGGAATGCCTCTCATTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

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### FIGURE 196

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742
```

```
><subunit 1 of 1, 148 aa, 1 stop
```

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLCWGPGGISGNKCLKMLQKREAPVPTKTKVAVDENKAKEFL

GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEY YGDYYORHYD

EDSAIGPRSPYGFRHGASVNYDDY

**Signal peptide:**

amino acids 1-30





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**FIGURE 198**

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM  
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRKFLNDSEQVARAWPHDT  
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS  
EPGPSGLEIGSLLLPLLLLLLLLLLWYCYQYRPFPLTATLGLAGFTLLLSLLAFAMYRP

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 195-217

**FIGURE 199**

GAGATTGGAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG  
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAAGTCTGCAAGACCCTAAGAACCATCAGCCC  
TCAGCTGCACCTCCTCCCCTCCAAGGATGACAAAGGCCTACTCATCTATTTGGTCAGCAGC  
TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT  
GGAGGACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGG  
AAAGCAAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGCGCTC  
TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCA  
CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGCAAGGCATCCACTGCGCAAAAAGGA  
TTGTGTCCGGAGCACGGGGGATGAACAACCTGGGTAGAATGGAGGTTGCACTGTTTCAGGCCGG  
CCACTCTCCTACTGGCTGACAGGATGCCGCCTGAGATGAAACAGGGTGCGGGTGACCCGTGG  
AGTCATTCCAAGACTCCTGTCTCACTCAGGGATTCTTCATTTCTTCTTCTTCTACTGCTCCA  
CTTCATGTTATTTTCTTCCCTTCCCATTTACAACATAAACTGACCAGAGCCCCAGGAATAAA  
TGGTTTTCTTGCTTCTCCTTACTCCCATCTGGACCCAGTCCCCTGGTTCCTGTCTGTTAT  
TTGTAAACTGAGGACCACAATAAAGAAATCTTTATATTTATCG



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## FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTACGCCCTGCTTGACTGAGAACCCA  
CCAGCTCATCCAGACACCTCATAGCAACCTATTATACAAAGGGGGAAAGAAACACCTGAG  
CAGAATGGAATCATTATTTTTTCCCAAGGAGAAAACCGGGTAAAGGGAGGGAAGCAATTC  
AATTTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCCAATTAAGAAATCCACTCAGAGAGGAC  
TTGGGGTGAACCTTGGGTCCTGTGGTTTTCTGATTGTAAGTGGGAAGCAGGTCTTGACACACGC  
TGTTGGCAATGTCAAGGACCAGGTTAAGTGACTGGCAGAAAAAATTCAGGTTGGAACAGCA  
ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC  
CTGTTGCATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATG  
CAGACTCCAGTTCTCTGCTGCTCCTGATGCTGGGATGCCCTCGTGATGTTGGTGGCGATGT  
TGCACCCCTCCCCACACACCTGCACCAGACTGTACAGCCCAAGCCAGCAGCAGCCCT  
GAAGCCAGGTACCGCTGGACTTTGGGGAATCCAGGATTGGGTACTGGAAGCTGAGGATGA  
GGGTGAAGAGTACAGCCCTCTGGAGGGCTGCCACCCCTTTATCTCACTGCGGGAGGATCAGC  
TGCTGGTGGCCGTGGCTTACCCAGGCCAGGAAGAACAGAGCCAGGGCAGGAGAGGTGGG  
AGCTACCGCCTCATCAAGCAGCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGACTGGG  
GGCTGATGAGGACGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTGACGCTTGGACCCAC  
GTGGCTCCAGGAGGCATCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCGAGGTGCGG  
CACCACCTGTGTCTGCAGCAGCACCCCTCAGGACAGCCTGCCACAGCCAGGCTCATCTCTG  
TTTCCATGATGAGGCTGGTCCACTCTCTGCGGACTGTACACAGCATCTCTGCACACAGTGC  
CCAGGGCCTTCTCTGAAGGAGATCCTCTGCTGGACGACCTCAGCCAGGAGGACAACCTAAG  
TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGTGAAGTTACTCAGGAGCAACAAGAG  
GCTGGTGCCATCAGGCCCGGATGCTGGGGGCCACAGAGCCACCGGGATGTGCTCGTCT  
TCATGGATGCCACTGCGAGGTGCCACCCAGGCTGGCTGGAGCCCCCTCTCAGCAGAATAGCT  
GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTA  
TTACCCCTCAAAGGACCTGCAGCGTGGGGTGTGGACTGGAAGCTGGATTTCCTCAGGGAAC  
CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATTAAGCCCCATCAGGAGCCCTGTG  
GTGCCGAGAGGAGTGGTGCCATGGACAGACATTACTCCAAAACACTGGAGCGTATGACTC  
TCTTATGTCTGCTGCGAGGTGGTGAACCTCGAAGTGTCTTCAAGGCCGTGGCTCTGTGGTG  
GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAAATCAGGATTCCCAT  
TCCCCCTCGACCAGGAGGCCACCTGAGGAACAGGTTTCGCATTGCTGAGACCTGGCTGGG  
GTCATTCAAAGAAACCTTTACAAAGCATAGCCAGAGGCCCTTCTCCTTGAGCAAGGCTGAGA  
AGCCAGACTGCATGGAACGCTTGACAGTGCAGGAGAGCTGGGTGTGCGGACATTCCACTGG  
TTTCTGGCTAATGTACCCCTGAGCTGTACCCATCTGAACCCAGGCCAGTTCCTCTGGAAAC  
GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAAGGGGACATCTTGGGCT  
GTCCCATGGTGTGGCTCCTTGCAAGTGAAGCCGGCAGCAACAGTACCTGCAGCAGCACAGC  
AGGAAGGAGATTCACTTTGGCAGCCCCACAGCACCTGTGCTTTGCTGTGAGGCAGGAGCAGGT  
GATTCTTCAGAACTGCACGGAGGAAGGCCCTGGCCATCCACAGCAGCACTGGGACTTCCAGG  
AGAATGGGATGATTGTCCAACTCTTTCTGGGAAATGCATGGGAAGCTTGGTGCAAGAAAC  
AATAAAGATTTGTACCTGCGTCCGTGTGATGGAAAAAGCCGCGCAGGTGGGCAATTTGACCA  
GATAAATGCTGTGATGAACGATGAATGTCAATGTCAAGGAAAAAGAGAAATTTGGCCATC  
AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATTTTCATGAAGCTGATCCTTTTGTGT  
GTGTGCTCCTTGTGTGTAGGAGAGAAAAAGCTCTATGAAGAATATAGGAAGTTTCTCCTTT  
TCACACCTTATTTCAATTGACTGCTGGCTGCTTA

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## **FIGURE 202**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760
><subunit 1 of 1, 639 aa, 1 stop
><MW: 73063, pI: 6.84, NX(S/T): 2
MLLRKRYRHRPCRLQFLLLLLLMLGCVLMMVAMLHPPHHTLHQTVAQASKHSPEARYRLDFG
ESQDWVLEAEDEGEEYSPLGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR
RQDKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRGLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVSP
VIDVIDWKTFAQYPSKDLQRGVLDWKLDHFWEPLPEHVRKALQSPISPIRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSEILPCSRVGHYQNDSSHPLDQEATL
RNRVRIAETWLGSKFETFYKHSPEAFSLSKAEKPCMERLQLQRRRLGCRTFHWFLANVYPEL
YPSEPRPSFSGKLHNTGLGLCADCAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP
QHLCFAVRQEQVILQNCTEEGLAIHQHWDQFQENGMIVHILSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER
```

**Signal peptide:**

amino acids 1-28

**FIGURE 203**

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACACAGCTGAGGAAGACCTCAGACATGGA  
 GTCCAGGATGTGGCCTGGCCTGCTGCTGTGCCACCTCCTCCCTCTCTGGCCACTGCTGTGTG  
 TGCCCTCCACCGCTGCTCAGGGCTCTTCATCCTCCCTCGAACCCACACGCCCGG  
 CGCCCCCGTGTGCCAGGGGAGGCCCCTCGGCCCCACGTATGTGTGCGTGTGGGAGCGAGC  
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCCAAGATCACGTTCGGCAAGTCTGCTGGCCACTG  
 CACCCCGACGCCACCCCATCAGGCTTTGAGGAGGGGGCCGCCCTCATCCCAATACCCCTGGGCT  
 ATCTGTGTGGGGTCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTGTCCAATCGCGG  
 ATTTCTGGACTATGTTTTTCAGCCCCCTCATGGGCTCGCAACCCCAACCCCAACTCAGACT  
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGGAGAGGCACCTGCCACCCTGCGGCCATT  
 CTGTTCGGGGGCGGTGGGAAGGTGTGGACCCCCAGCTCTATGTACAATTACCATTCTCCAT  
 CATCATTTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC  
 GACGCAGACCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGGCCAGCAGCCACTGACA  
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCTTCGGGGACTCACCTACCCCCACCCC  
 TGACCATGAGGAGCCCCGAGGGGACCCCGGCTGGGATGCCCCACCCCAAGGGGGCTCCAG  
 CTTTCCAGTTGAACCGGTGAGGGCAGGGGCAATGGGATGGGAGGGCAAAGAGGGAAGGCCAAC  
 TTAGCTTTTCAGAGCTGGGGTGGGGGTGCCCTCTGGATGGGTATGAGGAGGCAGGCGTGGC  
 CTCCACAGCCCCCTGGCCCTCCCAAGGGGGCTGGACCAGCTCCTCTCTGGGAGGCACCCCTC  
 CTCTCCCAGTCTCTCAGGATCTGTGTCTTATCTCTGCTGCCATAACTTCAACTCTGCCC  
 TCTTTGGTTTTTTTCTCATGCCACCTTGTCTAAGACAACCTGCCCCCTTAAACCTTGATTCCC  
 CCTCTTTGTCTTGAACCTTCCCCCTTCTATTCTGGCCTACCCCTTTGGTTCTCTGACTGTGCCCT  
 TCCCCTTCCCTCTCAGGATTCCTTGGTGAATCTGTGATGCCCCCAATGTTGGGTGAGGCC  
 AAGCAGGAGGCCAAGGGGCCGGCACAGCCCCATCCCACTGAGGGTGGGGCAGCTGTGGGGA  
 GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCTTGCACACCACCCGGAACACTCCCCAGCC  
 CCACGGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCCCTCACATATCTGTGACTTCG  
 GGTCCCTGTCCCCACCCCTTGTGCACTCACATGAAAGCCTTGCACACTCACCTCCACCTTCAC  
 AGGCATTTCGACACGCTCCTGCACCCCTCTCCCGTCCATACCGCTCCGCTCAGCTGACTCT  
 CATGTTCTCTCGTCTCACATTTGCACCTCTCCTTCCCACATTCTGTGCTCAGCTCACTCAG  
 TGGTCAGCGTTTCTGACACATTTACCTCTCATGTGCGTTTCCCGGCCCTGATGTTGTGGTGG  
 TGTGCGGCGTGCTCACTCTCTCCCTCATGAACACCCACCCACTCGTTTCCGCGAGCCCTGC  
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGCCCTCATCGGTCAATGG  
 TCTGCTCCCATCCACACATTTGTTTCTCTGTCTCCCACTACTCCAAGGATGCCGGCA  
 TCACCCCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCCAGACTTCACCCCCAGCCCA  
 CTGCTAAAAATCTGTTTTCTGACAGATGGGTTTTGGGGAGTCGCCTGTCTGCACATACATGAGAA  
 AGGGACTCCCAATTTGCCCTTCCCTTTCTCCTACAGTCCCTTTTGTCTGTCTGTCTGCTGGCT  
 TCTGTGTGTGTCATTTCTCTGCACTTCAGAGCCCCCTGAGCCAGTCCCTTCCCTCCAGCCCT  
 CCCTTTGGGCTCCCTCACTCCACTAGGCTGCCAGGGACGGATCAGCTGGTGTCAAGGCC  
 ATCGGGAGCTCTGCCTCCAAGTCTACCCCTTCCCTTCCCGGACTCCCTCCTGTCCCCTCCTTT  
 CCTCCCTCCTTCTCTCACTCTCCTTCTCTTTGCTTCCCTGCCCCTTCCCTCCCTCAAGGT  
 CTTCCTCCTTCTCACTGGTTTTTCCACCTTCTCTTCCCTTCTCCCTGGCTCCTAGGCT  
 GTGATATATATTTTTGTATATCTCTTCTTCTTCTGTGGTGATCATCTGAATTACTGTG  
 GGATGTAAGTTTCAAAATTTCAAAATAAGCCTTTGCAAGATAA

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## **FIGURE 204**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGFAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPGAV  
PGRDGSPGANVIPGTPGIPGRDGFKEGKGECLRESFEESWTFPNYKQCSWSSLNYGIDLGKIA  
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYYLDQGSPEMN  
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

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## FIGURE 205

GTAAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGGATGG  
 CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGGT  
 CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC  
 GTCGGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC  
 CAGCCCCACCGTCGCGCCAGGACCCGAGGACAGCACCAGCGCAGGAGCGGCTGGACCAGGGC  
 GGCGGGTCGCTGGGGCCCGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG  
 CGTGGTGCTGGCGCTCGTGGTCTCGCGCTGAGAAAGTTTTCTGCCTCCTGAAGCGAATAAA  
 GGGGCCGCGCCCGGCCGCGCGCGACTCGGCAAAAAAAAAAAAAA



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## **FIGURE 206**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGFVESTSPGREPVDTG
PPAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domain:**

amino acids 91-110

#### **Glycosaminoglycan attachment site.**

amino acids 44-47

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 116-119

#### **N-myristoylation site.**

amino acids 91-96

# **FIGURE 207**

GGCCGTTGGTTGGTGC GCGGCTGAAGGGTGTGGCGCAGCAGCGTCGTTGGTTGGCCGGCGG  
CGGGCCGGGACGGGCATGGCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCA  
CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATTGTGA  
ACTTCAAGTCTCTGGTGGTGGGCGACATCCCCGTGTCAGGGGCGCTGCTCACCAGCTGGAGC  
GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATACCCGGGAGAAGCTGGA  
CCAAGTGGCGACAGAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC  
CCGGGTATTTCCTCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC  
GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG  
ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGGGGACCTCCCCTAAGTAGCCCC  
CCAGAGGCGCTGGGAGTGTGGCACCGCCCTCCCTGAAGTTTGCTCCATCTCAGCTGGGG  
GTCAACCTGGGGACCCCTTCCCTCCGGCCATGGACACACATACATGAAAACAGGCGCAT  
CGACTGTGACGACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACATGCACAG  
ACTGCGACGTGCGCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT  
GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGAGGGGGGCTCCCCGCTTCCAC  
CTGGCTGTCTCGGGTAGGGCGGGGCGTGGGTTAGGGGCGCACCACTTCCAAGCCTGTGT  
CCCACAGGTCTCGGCGCAGTGGAAGTCACTGTCCAGGGCCTCCTGAATACATAAATAAC  
TGGCACAAGTAAGTCCCCCTCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG  
GGTGAGTATGTGTGGGGCAGAGGTGGCTCCCTCAGCTCCCACGTCTTAGAGGGGCTCCCGA  
GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGCTGCAGTCCCTTTCTCCCTCAAAG  
GTCTCCGACCCCTCAGCTGGAGGCGGGCATCTTTCCTAAAGGGTCCCCATAGGGTCTGGTTCC  
ACCCATCCCAAGCTGTGGTTCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC  
ATGGAGGGGCTGACTGCCCCGACATTGCCTTTTACAGACGACACGAGCATGAGTTAAGCGGC  
CCTGACCTGGACTTCAGGGGAGGGGGTAAAGGGAGAGAGGGGGGCTAGGGGGCTCTCT  
AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC  
CTCTGCAACCACACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG  
CCTGGGACACACAGAGCCACCCCGGCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA  
AGGGGTGCTCGTAAGCCAAACACGAGCTGCCGCGGCTGCACACCTTCCGACATCCCAGGC  
ACGAGGGTGTGCTGGATGTGGCCACACATAGGACCACACGTCCCAGCTGGGAGGAGAGCCT  
GGGGCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC  
CCGACGCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT  
TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCCAGGGCAAC  
GTGGGGCGGAGACTCAGCTGGACAGCCCCCTGCTGTCACTCTGGAGCTGGGTGCTGCTGC  
CTCAGGACCCCTCTCCGACCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG  
GAGGAATGGGGTGGGCTGTGCGCAGCATCAGCGCTGGGCAGGTCCGCAGAGCTGCGGGA  
TGTGATTAAAGTCCCTGATGTTTCTC

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**FIGURE 208**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

&gt;&lt;subunit 1 of 1, 157 aa, 1 stop

&gt;&lt;MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK

ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER

HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP

**Signal peptide:**

amino acids 1-15

**FIGURE 209**

AGCAGGAGCAGGAGAGGGGACAATGGAAGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTCTCT  
CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG  
GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATGTGCTGCC  
ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCA  
TAGCATGGTGCAAAAATCCCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGA  
CACACTACAACATCACTGGGAACACCATCTGCCTCTTTCGCCTGGTAGACAATGAACAACTG  
AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT  
CAACAGCCTCCACATGGTGACAGAGTACAACCTGTGACTGTGATTGGGTATTCAACAGCG  
TAATTCAGATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG  
CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG  
TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTCAAATAAAGGAGTCTCAACTGCCAG  
CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTTCC  
GTAGAGCATGTGCAAAACTTTTGTGATGGATTCCTAAGTGGAATAATTGTTGAAAGAAAATCG  
TGAATCAGAAGGAAAAGACTCCAAGGTGGAACCTCTGACTTCTCCTTGGAATAACATATGGCC  
AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACTCAAATCTCAGAGACACTAAACAACAG  
GATCACTAGGCCTGCCAACACACACACACGACGTGCACACACGCACGCACGCGTGCACAC  
ACACACGCGCACACACACACACACAGAGCTTCATTTCTGTCTTAAATCTCGTTTTCTC  
TTCTTCCTTCTTTTAAATTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATT  
CATACTCTGTAAGCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG  
CCTCTATGAAAGAGAGGCATTCTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGT  
TTGTATACTGCACATGACTTACACACAACATAGTTCTCTGCTCTTTTAAGGTTACCTAAGGGT  
TGAAACTCTACCTTCTTTTATAAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGG  
ATGGTTTTAAACACCTTTGTGAAATTGTCTTTTGGCAGAAGTTAAAGGCTGTCTCCAAGTC  
CCTGAACCTCAGCAGAAATAGACCATGTGAAACTCCATGCTTGGTTAGCATCTCCAACCTCC  
TATGTAAATCAACAACCTGCATAATAATAAAAGGCAATCATGTTATA

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## **FIGURE 210**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLFLLTCELAEEVAAEVEKSSDGPAAQEPTWLTDPAAMEFIAATEVAVIG  
FFQDLEIPAVFILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRLLVDNEQLNLEDEDI  
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLIMNKASPEYEENMHRYQKAA  
KLFQGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVQNF  
CDGFLSGKLLKENRESEGKTPKVEL

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 143-162

GCGAGACGCCGCGCTGGGACCGGAGTGGGGAGCGCGCGCTGGAGGTGCCACCCGGCGCGGGTG  
GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG  
GACGCGGGCGGCGCGGCGGCGACTGCAGTGGCTGGACCATGGCAGCGTCCGCCGGAAGCCGGG  
GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTGGTGGTGGCGGCGCGCTTGG  
GCTCTTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA  
ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC  
TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTAGTGTGTTTTCCTACTACTC  
CCAAGGGCAAGGTGTACCTTGGGAATTTACCCATTTAAAGCAGAACTCAGCTGGGCTGGAG  
ACCTTGACAAGAAAGATGCATCAATCAACATGAAAAATATGCAGTTTATACACAAATGGCACC  
TATATCTGTGATGTCAAAAACCCCTCTGCATCGTTGTCCAGCCTGGACACATTAGGCTCTA  
TGTGCTAGAAAAAGAGAAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG  
CTGTGGTCTTAGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAA  
AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTCAACAGTTAAGCAGGC  
TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC  
AGGGCCAGTCATATATGCACAGTTAGACCACCTCCGCGGGACATCAGTGCACAGATTAAC  
AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAATTAAGAGAATACCTAGAACATATC  
CTCAGCAAGAAACAAACCAAACTGGACTCTCGTGCAGAAAATGTAGCCCATACCACATGT  
AGCCTTGGAGACCTCAGGCAAGGACAAGTACAGTGTACTCAGAGGGAGAGAAAGATGTGT  
ACAAAGGATATGTATAAATATCTTATTAGTCACTCGTATGAGAGGCCAGTGTGTCATGA  
TGAAAGATGGTATGATTCTAÇATATGTACCATTGTCTTGCTGTTTTTGTACTTCTCTTTT  
AGGTCAATTACAAATTTGGGAGATTTCAGAAACATTCCTTTCACCATCATTAGAAATGGTTTG  
CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG  
GGCTTAAGACTGATTAGTCTTAGCATTCTAGTGTAGTGGAGGATGGAGATGCTATGATGGAA  
GCATACCCAGGGTGGCCTTTAGCAGAGTATCAGTACATTATTTGTCTGCCGCTTTTAAAA  
AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT  
AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCCTTG  
AAATGTGTCAATCAATTTCTGGATTCTAATAGCAAGATAGCAAAAGGATAAATGCCGAAG  
GTCACTCAATTCTGGACACCTGGATCAATACTGATTAAAGTAAAAATCCAGCTTTTGCTT  
GAGAAGTTTTGTAACTGGAGAGTAAAAAGTATCGGTTTTA

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## **FIGURE 212**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS  
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKASINIEN  
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI  
LAVLYRRKNKSRDYGTCSTSESLSPPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG  
GHHSDKINKSESVVYADIRKN

### **Signal peptide:**

amino acids 1-37

### **Transmembrane domain:**

amino acids 161-183

**FIGURE 213**

GCCGGCTGTGCAGAGACGCC**ATGT**ACCGGCTCCTGTGCAGCAGTGACTGCCCGGGCTGCCGCC  
 CCCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGTCCATCAGCGCGCCGGGCTGCCGCC  
 TCTCGGCCACGGCTGGGTGCGGGGCTCGGGTGGGGCTGGGGCTGGGCTCGGGGTGAAGC  
 TGGCAGGTGGGCTGAGGGGCGCGGCCCGCGCAGTCCCCCGCGGCCCGACCTGAGGCG  
 TCGCCTCTGGCCGAGCGGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCGGC  
 GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA  
 TCAAGGATGAGGTGGGCGCACCGGCATAGTGTTGGAGTTTCTGTAGATGGAAGAAGTC  
 TGGTCAGAAAGTTTAGGTTATGCTGATGTTGAGAACCGTGACCATGTAAACCAGAGACAGT  
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG  
 CAGGGAAACTGGATCTTGATATTCAGTACAACATTATGTTCCCGAATTCCAGAAAAAGAA  
 TATGAAGGTGAAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGGAATTCG  
 TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAGCCTTGAAGATGA  
 TGAAAGAGAATGTTGCATTTGAGCAAGAAAAAGAAGGCCAAAAGTAATGAAAAGAATGATTTT  
 ACTAAATTTAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAAACCTGGCAAGAA  
 AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAGTTGAAAATTCAATTGAAT  
 CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA  
 ACTTTTGGCTATACCCTACTGGCAGCCATAGTAGAGAGAGCTCAGGATGTAATATTTGGA  
 CTATATGCAGAAAATATCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC  
 CAGTGATTACAAATAGAGCAAGG**TAA**ATGAATACCTTCTGCTGTGTCTAGCTATATCGCATC  
 TTAACACTATTTTATTAATTAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC  
 CACATTTTGGGAGCTTTTCTACATGTCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAACA  
 TGTTTATAAAGTAAAAAA



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## **FIGURE 214**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGGLGLGLALGVKLAGGLRG  
 AAPAQSPAAPDPEASPLAEPPEQESLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA  
 PGIVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLTMVALAKLWEAGKLDLD  
 IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF  
 EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN  
 DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPVIYNRAR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 39-60

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## FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG  
 AGGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC  
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGCAGCGGCTGCCGGGCCGGGACT  
 GGTGCGCGAGGGGCTGGGGCGAAGGTCGAGAGGGCGAGGCCCTGTGGCACGGTGGGGCTGCT  
 GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT  
 GGAACCAGCAGGATGGTACCTTGTCCCTGTCACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC  
 CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG  
 GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG  
 TGGAGTCGCACCTGTGCGGACCAGCTGACCCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC  
 GTGTCGGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA  
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG  
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCAGAGGCCAAGAACCCCAAGGAGCAGAAG  
 TCCTTCTTCGCCAATACTGGATGTACATCATTCCCGTCGTCTGTTCCTCATGATGTCAGG  
 AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC  
 TTTGCTGTGTGCCACCCTCCCTGTAAAGTCTATTTAAAAACATCGACGATACATTGAAATGTG  
 TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG  
 TCCTGATGTACAAGCTTGATTGAAATTCAGTCTCACTTGATACGTTATTCAGAAACCCAAG  
 GAATGGCTGTCCCATCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT  
 TAAACTGTCCCCCAGATCGACACGCAAAAAAAA

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## **FIGURE 216**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529

><subunit 1 of 1, 269 aa, 1 stop

><MW: 28004, pI: 5.80, NX(S/T): 1

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI  
 DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGLRDVAALNGLYRVRIPRRPGALDGLEA  
 GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ  
 LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEKSFFAKYWYIIIPVVLFLMSGAPDTGGQ  
 GGGGGGGGGGSGLCVPPSL

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 226-243

**FIGURE 217**

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCC  
 GGAGCCGGACGTGTCCGGGGCGTCCCGCAGACCGGGGCAGCAGGTCGTCCGGGGGCCACC  
**ATG**CTGGTGACTGCCTACCTTGCTTTTGTAGGCCCTCCTGGCCTCCTGCCTGGGGCTGGAAC  
 GTCAAGATGCCGGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCTTCGGTTTC  
 AACTGGACTTCTATCAGGTCTACTTCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC  
 CTCTATAAACTCTACCAGATTACTACTTCTGGAAGGTCAAATTGCCATCCTCTATGTCTG  
 TGGCCTTGCCCTCTACAGTCCTCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTC  
 GCAAGAATTCTTGTGTCCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAACTCTCT  
 CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT  
 CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT  
 GGATCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT  
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC  
 CATCCCTCTCCTGGCTCTGGCAGGGGCCTTGGCCCTTCGAAACTGGGGGGAGAACTATGACC  
 GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGTGCGGACGCCGC  
 GTGCTGCTGCTGGGCACCATAACAAGCTCTATTGAGAGTGTATCTTCATCTTTGTCTTCCT  
 CTGGACACCTGTGCTGGACCCACACGGGGCCCTCTGGGCATTATCTTCTCCAGCTTCATGG  
 CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG  
 CCCATGCACCTGCTGTCCCTTGCTGTGCTCATCGTCGTCTTCTCTCTTCATGTTGACTTT  
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCCTTCATAGCCTTTCTACTTATTGAGT  
 TGGCTTGTGGATTATACCTTTCCAGCATGAGCTTCCTACGGAGAAAGGTGATCCCTGAGACA  
 GAGCAGGCTGGTGTACTCAACTGGTTCGGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT  
 CCTTGCTCCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTACGATTTGCTCTG  
 CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTACCCTGGTAAGGCATGATGCT  
 GAGCTGCGGGTACCTTCACCTACTGAGGAGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG  
 GACAAGATAGCTGGGACAGACTCTTGAATTCAGCTATCCGGGATTGTACAGATCTCTCTGT  
 GACTGACTTTGTGACTGTCTGTGGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA  
 TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAAGTCCCTCTGTGTTACTCCATTTAGAAA  
 ATAAACACTTTTAAATGATCAAAAAAAAAA

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## **FIGURE 218**

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY  
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS  
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG  
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR  
VLLGLTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFFSSFMAASLLGSSLYRIATSKRYHLQ  
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVI PET  
EQAGVLNWFRVPLHSLACLGLLVLHSDRKTGTRNMFISCSAVMMALLAVVGLFTVVRHDA  
ELRVPSPTTEEPYAPEL

### **Signal peptide:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,  
314-330, 343-359, 379-394, 410-430

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## FIGURE 219

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCGGGGCCGGGCCCGCCCTGGAGATG  
 GTCCCCGGCGCGCGGGGTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCCA  
 CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTTCGATACA  
 TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT  
 CACCTTGTCGCCGCTGAACCTCCAGAGGCCTGCGGGGAAGTCAAGCGTTTCTTCATCCA  
 GGACCAGATTGCTCTGGTGGAGAGGGGGGCTGCTCCTTCTCTCCAAGACTCGGGTGGTCC  
 AGGAGCACGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC  
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCTCTGCTCGG  
 CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT  
 CCATCCCAGTCAATGTCAACAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC  
 TGGTAGAAGAGTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC  
 AGGAATTTTGCTACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA  
 AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACCACTGGCCTTCCCTTCCCAGG  
 GCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA  
 GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT  
 CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG  
 AGTGGTTTAAAGAGCTGGTGGTTTGGGGACTCAATAAACCCCTACTGACTTTTTCAGCAATAAA  
 GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 220**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ  
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVNDNSF  
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

**Signal peptide:**

amino acids 1-20

[illegible]



**FIGURE 222**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538

><subunit 1 of 1, 116 aa, 1 stop

><MW: 12910, pI: 6.41, NX(S/T): 1

MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGCHCGLGGRGQPKDATDW

CCQTHDCCYDHLKTQCGGIYKDNKSSIHCMDSLQRYCLMAVFNVIYLENEDSE

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 1-24

**N-glycosylation site.**

amino acids 86-89

**N-myristoylation sites.**

amino acids 20-25, 45-50

**Phospholipase A2 histidine active site.**

amino acids 63-70

**FIGURE 223**

CTCGCTTCTTCCTTCTGGATGGGGGCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAG  
GGTGCCCGGCACAACCAGACGCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGG  
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT  
GGCCCTGGAGGAGGCAAGTATTTCAGCACCACTGAAGACTACGACCATGAAATCACAGGGCT  
GCGGGTGTCTGTAGGTCTTCTCCTGGTAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGG  
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCTGCGAGCCAGGCGAATAC  
ATCACAAAAGTCTTTGTCGCCTTCCAAGCTTTCTCCGGGGTATGGTCATGTACACCAGCAA  
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAG  
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTTGGC  
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC  
AGCAAACCTACCCGTGGGTCGC**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT  
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA  
AATAAAGCTTCTGCAGAAA

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## **FIGURE 224**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541

><subunit 1 of 1, 178 aa, 1 stop

><MW: 19600, pI: 5.89, NX(S/T): 1

MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK  
 LGDSWDVKLGALGGNTQEVTLPGEYITKVVFVAFQAFLRGMVMTSKDRYFYFGKLDGQISS  
 AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR

**Signal peptide:**

amino acids 1-22

**FIGURE 225**

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT  
 GAACGGGTGCTCATCACGGGAACCTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG  
 CCCCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTT  
 TTTTTTTAAACGCCCCCTCCCCACCCCCAAAAAACTGTAAAGATGCAAAAACGTAATAT  
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATCGCGGTGTGGGATT  
 TATTTGTTCTTGGAGTGTTCTGCTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT  
 CCAAAGGGTCCAATTTTTCTCTGGGTGTGACGAGCCCTGACTCACTACAGTGCAGCTG  
 ACAGGGGCTGTGATGCAACTGGCCCTTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTTGAA  
 CAATACAAAGG**ATG**GGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTTAGCACTGGTT  
 ATAGCCCCACTGTCTTACTGACAATGCTTCTTCTGCGCAACGAGGATGCCTTAAGGGGTG  
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTA  
 TATCTGCTGGTTGCTTAGGTTTGTCCTTCGCTATAACAGCCTTCAAAACTTAAGTATAAT  
 CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT  
 TGACGAAAATGCTTTTAAATGGAATACGACAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA  
 TCTCCTATTTTCTTAAACAATACCTTCAGACCTGTGACAAATTTACGGAATCTGGATCTGTCC  
 TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTCGGGAAGCTGCTGAGTTT  
 ACATTTACGGTCTAACTCCCTGGAACCATCCCTGTGCGAATATTTCCAAGACTGCGCGAACCC  
 TGGAACTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC  
 ATGATCAGACTCAAAGAACTTCACCTGGAGCACAAATCAATTTTCCAAGCTCAACCTGGCCCT  
 TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGGAATAAAAATCAGTGTCTATAG  
 GACAGACCATGCTCGGACCTGGAGCTCCTTACAAGGCTTGATTATCAGGCAATGAGATC  
 GAAGCTTTTCACTGGACCCAGTGTTTTCCAGTGTGTGCCGAATCTGCAGCGCCTCAACCTGGA  
 TTCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGATATCCCTCAATGACA  
 TCAGTCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTGCTCCCTTGTAAACTGGCTG  
 AAAAGTTTTAAAGGTTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG  
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGT  
 TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAAGCCCAAGCTCCCGAGGCCGAAGCAT  
 GAGAGCAAAACCCCTTTGCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC  
 TGACGCCGAGCACATCTCTTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCG  
 TGCTCGTCATCTGCTGGTTATCTACGTGTCTGGAAGCGGTACCTGCGAGCATGAAGCAG  
 CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAGACAGTCCCTAAAGCAAT  
 GACTCCAGCAGCCAGGAATTTTATGTAGATTATAAACCCACCAACACGGAGACCGGAGA  
 TGCTGCTGAATGGGACGGGACCCCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA  
**TGA**ACCATTGTGATAAAAAGAGCTCTTAAAGCTGGGAAATAGTGGTGCTTTATTGAACCT  
 TGGTGACTATCAAGGGAACCGGATGCCCCCTTCCCTTCTCCCTCTCACTTTGGTGG  
 CAAGATCCCTTCTTGTCCGTTTTAGTGCATTATAATACTGGTCATTTTCCCTCTCATACATA  
 ATCAACCCATTGAATTTAAATACCACAATCAATGTGAAGCTTGAATCCGGTTTAAATATAA  
 TACCTATTGTATAAGACCCCTTTACTGATTCCATTAATGTGCACTTTGTTTTAAGATAAAACT  
 TCTTTCATAGGTAAAAA

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## **FIGURE 226**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTLLTMLSSAERGCPCGCRCEGKMVYCESQKLQEI PSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVNTLRNLDLSYNQLHSLGSEQFRGLRKLSSLHLRSNSLRTIPVRI FQDCRNLELL
DLGYNRIRSLARNV FAGMIRLKE LHLEHNQFSKLNLA LFPRLVSLQNL YLQWNKISVIGQTM
SWTWSSLQRLDL SGNEIEAFSGPSVFQCVPNLQRLNLD SNKLTFIGQEILDSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTI ICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADA EHISFHKI IAGSVALFLSVLVI
LLVIYVSWKRPY PASMKQLQQRSLMRRHRKKRQSLKQMPSTQEFYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

## **FIGURE 227**

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACTACTATCCTAAGTTGACTGTCCTT  
TAAAT**ATGT**CAAGATCCAGACTTTTCAGTGTCACCTCAGCGATCTCAACGATAGGGATCTTG  
TGTTTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT  
AAATTATAATGACCAACACCCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG  
TGGCAGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCGA  
ATTGATTCTCAGGGCGACCATGGCAGTTTTTGCTGTTGGAGACTTGGACTCTATTTATGG  
GACAGAAGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT  
ATCCTGTTCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA  
AAAACAACCT**TGA**TTTTAGTGTTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA  
AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTATATA  
GTCTGAGGAAGGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATG  
TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC  
AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT  
TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC  
CTAGCATGGGGTCCATAAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT  
GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA  
GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT  
CAGCAAAAACAAGAGGTTTTATGCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA  
AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC  
CTTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTCTCTGAGCCTCAGGGCTTG  
GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC  
AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA  
CAAAAACATCCATCACAGATGACATATGATCTTCAGTGACAAATTTGTTGAACAAAACAAT  
AAACATCAATAGATATCTAAAAA

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## **FIGURE 228**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303
><subunit 1 of 1, 146 aa, 1 stop
><MW: 16116, pI: 4.99, NX(S/T): 0
MSRSRLFSVTSIAISTIGILCLPLFQLVLSDLPCCEEDCMVNYNDQHPNGWYIWILLLLVLVA
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP
VPAPCFGLGSPPPYEIVKTT
```

### **Signal peptide:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 52-70

**FIGURE 229**

GAGCGGAGTAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT  
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGAGCTGACGCCCGCTTATTA  
 GCTCTCGTTCGCTCGCCCCGGCTCAGAAGCTCCGTGGCGGCGGCGACCGTGACGAGAAGCCC  
 ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAAACT  
 CCCTCTTCAAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACACCTTGTCTGAAG  
 ATGAAGAATATACAAATATTGAGGATATTTTTTCTTTTTTTTCAAGCTTGATTGTGGC  
 TTACCTCAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTGTTGCTTCTTCAGAAATGTTTTTA  
 CAATCTCAAGAAAAATATGTCCCGAGAAATTGAGTTTACTGTTGCTTGTATTGGAAGTCAAT  
 TGGGGATTGATGTTTACTGCACATACCTTTTCAACCAAGACATCAAAGCAGTGTCAAGTT  
 ACGTGAGCAAACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGA  
 ACACAGTGGATGTCGAGAACGGTGTCTTCTATGGCAGGATCTGCGGATCTGAAAAGAACAAT  
 GCTGTCCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAGTTGACTATAT  
 TGTGTGTAATGGCTCAGCAGCCAAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA  
 CCACAAATAAAAGAACGAATGCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGTGC  
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC  
 AGAGCAATACITTTACAATAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTTCATGGAAC  
 TCTAATTCTGTACATAAAAATTTTAAAGTTATTTGTTTGCTTTACGGCAAGCTGTTCAATG  
 CTGTACTATGTCCTTAAAGAGAATTTGGTAACTGGTGTGATGTGGTAAGCAGATAGGTGAGT  
 TTTGTATAAACTTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTTC  
 ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTGGACAAGTGAAGAAATGTTAA  
 TCATTCTGTCATTTGTTCTCAATAGATGTAACCTGTAGACTACGGCTATTTGAAAAATGTG  
 CTTATTGTACTATATTTTGTATTCCAAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA  
 TAATGTTTTGAAATCATGCCCCAAGAATGTATTGATTTGCACATTCCTTCAGAAATACTGA  
 AGGTTAATTATTGTATATTTTAAAAATTACACTTATAAGAGTATACTTGAATGTAATATAA  
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAAAAAGTT  
 GTAAACTCTAATCTTATACTTATTGAAGAATAAAGATATTTTTATGATGAGAGTAACAATA  
 AAGTATTTCATGATTTTTCACATACATGAATGTTTCATTTAAAAGTTTAATCCTTTGAGTGTCT  
 ATGCTATCAGGAAAGCACATTTATTTCCATATTTGGGTTAATTTTGCTTTTATTATATTGGTC  
 TAGGAGGAAGGGACTTTGGAGAATGGAACCTTGAGGACTTTAGCCAGGTGTATATAATAA  
 GGTACTTTTGTGCTGCATTAAATTGCTTGGAAAGTGTTAACATTATATTATATAAGAGTATC  
 CTTTATGAAATTTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC  
 TTAATAATAAGAACATTTAAAAATATAAATCATGAAGATTGACTATCTTTTCAGGAAAAAAGCT  
 GTATATAGCAGGGAACCCCTAATCTTGGGTAAATCTAGTATATAAACAATATACTTTTAT  
 TTAATTTCCCTTGTAGCAAACTAATTGGCCACATGGTGCCCTATTTTCATAGTATTTATT  
 CTCATAGTAACTGCTTAAGTGCAGCTAGCTTCTAGATTTAGACTATATAGAATTTAGATAT  
 TGTATTGTTTCGTCATTATAATTATGCTACCACATGTAGCAATAATTACAATTTTTATTAAAA  
 TAAATATGTGAATAATTGTTTATGTAAGACAGATTTCCAAATCTCTTCTCTTCTCTGTA  
 CTGCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGT



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## **FIGURE 230**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTNGTSGNL
VPVTTNKRTNVSGSIR
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

# FIGURE 231

CGCGGCCGGGGCCGCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC  
**CATG**CCGTGGCCCCGTGCTGCTGCTGCTGGCCGTGAGTGGGGCCAGACAACCCGGCCATGCT  
TCCCCGGGTGCCAATTGCGAGGTGGAGACCTTCGGCCCTTTTCGACAGCTTCAGCCTGACTCGG  
GTGGATTGTAGCGGCTGGGGCCCCACATCATGCCGGTGCCCATCCCTCTGGACACAGCCCA  
CTTGGACCTGTCCTCCAACCGGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGGCCGGGCT  
ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCCTACCTGCC  
TTCTCCCGCCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC  
AGCCGAGAGCTTACCAGCTCACCCTTGAGCGACGTGAACCTTAGCCACAACAGCTCCGGG  
AGGTCTCAGTGTCTGCCTTACGACGACAGTCAGGGCCGGGCACTACACGTGGACCTCTCC  
CACAACCTCATTCACCGCCTCGTGCCCCACCCACGAGGGCCGGCCTGCCTGCGCCCAACCAT  
TCAGAGCCTGAACCTGGCCTGGAAACCGGCTCCATGCCGTGCCAACCTCCGAGACTTGCCCC  
TGCCTACCTGAGCCTGGATGGGAACCTCTAGCTGTCATTGGTCCGGGTGCCTTCGCGGGG  
CTGGGAGGCCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG  
TGGCTTCCGTGAGCTACCGGGCCTGCAAGTCTGAGCTGTGCGGGCAACCCCAAGCTTAACT  
GGGACAGGCTGAGGTGTTTTCAGGCCCTGAGCTCCCTGCAAGGAGCTGGACCTTTCGGGCAAC  
AACCTGGTGCCCTGCTGAGGGCCTGCTCCTTCCACCTCCCGGCACTGCAGAGCGTCAGCGT  
GGGCCAGGATGTGCGGTGCCGGCGCCTGGTGCGGGAGGGCACTACCCCGGAGGCCTGGCT  
CCAGCCCCAAGGTGCCCTTGCACTGCGCTAGACACCCGGGAATCTGCTGCCAGGGGCCCAAC  
ATCTTCT**GC**ACAAATGGTGTGGCCAGGGCCACATAACAGACTGCTGTCTGGGTGCTCTCAG  
GTCGCCGAGTAACTTATGTTCAATGTGCCAACACCACTGGGGAGCCCGCAGGCCTATGTGGCA  
GCGTACACACAGGAGTGTGGGCTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC  
AAAGTCTACCCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGAGCTTCGATGCCA  
AACCAGACTCGGGTCCCCCTCCTGCTTCCCTTCCCCACTTATCCCCCAAGTGCTTCCCTCAT  
GCCTGGGCGGCGCTGACCCGCAATGGGCAGAGGGTGGGTGGGACCCCTGCTGCAGGGCAGA  
GTTACGGTCCACTGGGCTGAGTGTCCCTTGGGCCATGGCCCACTACTCAGGGGCGAGTT  
TCTTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCCGCTTCATCCTTTTCTAT  
TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAGAATCAAGTCCACCTTCTCATGTGAC  
AGATGGGGAACCTGAGGCGCTTGAGAAGGAAAAAGGCTAATCTAAGTTCCTGCGGGCAGTGGC  
ATGACTGGAGCACAGCCTCCTGCCTCCAGCCCGGACCCCAATGCACCTTTCTTGCTCCTCTA  
ATAAGCCCCACCTTCCCGCCTGGGCTCCCTTGCTGCCCTTGCTGTCTCCCATAGCAC  
GAGTAGAGCAGCAGGACAGGCAAGAGCCTCACAAAGTGGGCACTCTGGGCCTTGACAGCT  
GTGGCGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCAGCTGGTT  
CCAGCCTAGCCAGTTTCTCACCCTGGGTGGGGTCCCCAGCAGCTCAGAGCTGGAACCTAC  
CATTCTCCCTGAGCATCTCTAGATGCTGCCCAAGGAGTGTGCTGAGTCTCTGGAGCTCA  
TCTGGCTGGGATCTCAAGGGGCTCCTGGATTCACTCCCACTGGCCCTGAGCACGACAGC  
CCTTCTTACCCTCCCAGGAATGCCGTGAAAGGAGACAAGGCTTGCCCGACCCATGTCTATGC  
TCTACCCCAAGGCGAGCATCTCAGCTTGCCAACCCTGGGCTGTTTCTTAGTCTTCATTTTA  
TAAAGTTGTGCTTTTAAACGGAGTGCTACTTTCAACCGGCTCCCTTACCCTGCTGGC  
CGGGGATGGAGACATGTCATTTGTAAAGCAGAAAAAGGTTGCATTGTGTTCACTTTTGTAA  
ATTGTCCTGGGCTGTGTTGGGGTGTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC  
AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGCTTCCCCACCTGCTTAGC  
CCATCTCTATCAACCGGCTCCTTGATTTAATAAACACTATAAAGGTTTAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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# **FIGURE 232**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLLAVSGAQTTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAGLGGLTHLSLASLQRLPELAPS
GFRELPGQLVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL
```

## **Signal peptide:**

amino acids 1-16

## **Transmembrane domains:**

amino acids 215-232, 287-304

**FIGURE 233**

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCGTGGGTCTGAGG  
 GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCA  
 AAACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT  
 GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC  
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTCTTAC  
 GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAAGCCTAAGATGAAAGCC  
 TCTAGTCTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG  
 ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG  
 GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAACATTGACATCAGAATCTTA  
 AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT  
 GCTAAGACTCTATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCC  
 GGAAGATCAGCAGCCTCGCCAATTCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT  
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA  
 CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAC TAGACATTCTTC  
 TGCAATGGATGGAGGAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTGAGGT  
 CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACACCATCTCTTTACT  
 GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCCTCCTTGCATGAT  
 TGTCCTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTTTGTAAATATCTT  
 TCTGCTATTGGATATATTTATAGTTAATATATTTATTTATTTTTTGTATTTAATGTATTT  
 ATTTTTTTTACTTGGACATGAAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG  
 AGCAGGTGATGTATTTTATACAGTAAAAAAAAAAACCTTGTAATTTCTAGAAGAGTGGCT  
 AGGGGGTTATTCTATTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA  
 TATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATT  
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATATAATTGTGTAT  
 CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA  
 CCAAAAAAAAAAAAAAAAAA

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## **FIGURE 234**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop .
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNGGATTCATNSHSDSELRP
EIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSFLLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG
ELDILLQWMEETE
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

**FIGURE 235**

CCGTTATCGTCTTGCGCTACTGCTG**AATG**TCCGTCCTCCGAGGAGGAGGAGAGGCTTTTGCCG  
CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC  
CGAGCTAGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG  
CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA  
GCCCAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT  
TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG  
TGTTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAAATCAGTCATTGGAGGGATGATG  
GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAATGACCTAGTGAAGGTTGAGATGCAAAT  
GGAAGGAAAAAGGAACTGGAAGGAAAACCATTGCGATTTTCGTGGTGACATCATGCATTTG  
CAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA  
AGAGCAGCACTGGTGAATATGGGAGATTTAACCCTTATGATACAGTGAACACTACTTGGT  
ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC  
TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAAGCAGAATAATGAATCAACCA  
CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTGAGGCTGT  
TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTTTACCATCTTGCTGAGAATGACCC  
CTTGGTCAATGGTGTTCTGGCTTACTTATGAAAAATCAGAGAGATGAGTGGAGTCAGTCCA  
**TTTTAA**

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## **FIGURE 236**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGA
RESAPYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGRMVITYEHLREVVFGESEDEH
YPLWKSIVIGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGGKPLRFRGVHHAFKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVNTPLEDNIMTHGLSSLCSGLVASILGTP
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT
YEKIREMSGVSPF
```

### **Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

# FIGURE 237

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC  
GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC  
TTAAGAAGTAAAAATGGCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG  
ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCGAGGTATATTGTTTTTACAGGC  
TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT  
TCACACATGTGGTGTATTTCCACATTGGCTTCTTCATGATAAATGCTGTATCCAATGCTC  
AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTAGGAAGAACAGGTGCTCGAGTTTGGCTT  
TTCATTGGTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTGGTG  
ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAATGCACCTTA  
TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCAGAGCTATGGACCTGAGATCAC  
TTCTTAAGTCACATTTTCCTTTTGTTATATTCTGTTTGATAGTAGGTTTTTATCTCTCAGT  
ACACATTGCCAAATGGAGTAGATTGTACATTAATGTTTTGTTTCTTTACATTTTTATGTTT  
TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTCATGTGCATAGACTGTTAATATGTA  
TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTATCTGAGATTTAGAA  
CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAGTAACCACTCTTGT  
CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGG  
CCGATTGCTTGAGGTCAAGTGTTGAGACCAGCCTGGCCAACATGGCGAAACCCATCTACT  
AAAAATACAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCAGCTACCTGGGAGGC  
TGAGGCAGGAGAATCGCTTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC  
TGCACTCTAGCCTGGGGGAGAAAGTGAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC  
TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA  
TAAAAGTTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTTGGTAAGA  
AAAAATATTGTTCTTATGTATTGAAGAAGGTACTTTTATATAATGATTTTTTAAATGCC  
AAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTAATATGACTTTATGTGAGAA



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## **FIGURE 238**

MAGFLDNFRWPECECIDWSERRNAVASVVGILFFTGWIMIDAADVYPKPEQLNHAFHTCG  
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ  
NTDVYPGLAVFFQNALIFFSTLIYKFG RTEELWT

**Important features:**

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 23-42 (type II), 60-80, 97-117, 128-148

**FIGURE 239**

GTTGATGGCAAACCTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA  
 CTGGCGGCCCGCAACACTCCGTCTCACCTCTGGGCCACTGCATCTAGAGGAGGGCCGTCT  
 GTGAGGCCACTACCCCTCCAGCAAAGTGGGAGGTGGGACTGTCAGAAGCTGGCCAGGGTGGT  
 GGTGAGCTGGGTGAGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG  
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGAAGCTGACCCCAAGCCACCTTCACCTGGACAG  
GATGAGAGTGTGAGGTGTGCTTCGCCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA  
 TGTTTATTGGAAGCTACATGAGCTTCAGCATGAAAACCATCCGCTCTGCCACGCTGGCTGGCA  
 GCCTCGCCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCC  
 AGCCAACACTACTTTGCGTTTAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT  
 GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCATAACATC  
 GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG  
 AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATTCGGGGGGTGCAGTGGTGTGGTGG  
 CCTCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTTCTGACTTG  
 GGGAGTTCCTACGAAAAACAACCTGGGCTTCCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA  
 CCTCAGGGGTAAAGCCCTTTGAGCAGTTCCTTAAAGAACAGCCAGACACAAACAAATACG  
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTTAGGGTGGC  
 TGTGGCTCTTCTCAGCCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG  
 GCAGGGGCTGAGGAGGAGAGCAGGGGTGCTGCGTGGAAAGGTGCTGCAGGTCTTGACGC  
 TGTGTCGCGCCTCTCCTCTCGGAAACAGAACCTCCACAGCACATCTACCCGGAAGACC  
 AGCCTCAGAGGGTCCTTCTGGAACAGCTGTCTGTGGAGAGAATGGGGTGCTTTTCGTCAGGG  
 ACTGCTGACGGCTGGTCTGAGGAAGGACAAACTGCCAGACTTGAGCCCAATTAAATTTTA  
 TTTTGTGCTGTTTGAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 240**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMTIRLPRWLAASPTKEIQVKYKCGLIKPCP  
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG  
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRLKFSDLGSSYAKQLGFRDSWVFIGAKD  
LRGKSPFEQFLKNSPDTNKEYEGWPELLEMEGCMPPKPF

### **Important features:**

#### **Signal peptide:**

amino acids 1-15

#### **ATP/GTP-binding site motif A (P-loop).**

amino acids 184-191

#### **N-glycosylation site.**

amino acids 107-110

**FIGURE 241**

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGCTCCTGGGGAT  
CCAGAAACCCATGATACCCCTACTGAACACCGAATCCCCCTGGAAGCCACAGAGACAGAGACA  
GCAAGAGAAGCAGAGATAAATACACTCAGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTCTC  
TCACTCCTCCCTCCCTCTCTCTCTGCTGTCTAGTCTCTAGTCTCAAATTCACAGTCCC  
CTGCACCCCTTCTCTGGGACACTATGTTGTTCTCCGCCCTCTGCTGGAGGTGATTGGGATCC  
TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGGCCA  
GCCTCTTACCTGAGTGTGAAACAATGCCAGTCGCCCATCGATATTAGACAGACAGTGT  
GACATTTGACCCTGATTTGCCTGTCTGCAGCCCCACGGATATGACCAGCCTGGCACCAGC  
CTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCCCTACCCCTGTATCTG  
GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC  
CCCAGGGGGTTCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC  
ATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCCTCAGGGCCTGGCT  
GTCTTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTTCTGAG  
TCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAG  
AGCTGCTCCCCAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT  
TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCT  
GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA  
ACTACCAGGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTTCATCCAAGCAGGA  
TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG  
CCTTCTCCTGGCTGTTTATTTTCATTGCTAGAAAGATTTCGAAGAAGAGGCTGGAAAACCGAA  
AGAGTGTGGTCTTCACCTCAGCACAAAGCCACGACTGAGGCATAAAATTCCTTCTCAGATACCA  
TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTG  
GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCTGGACATCTCTTAGAGAG  
GAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGANCAAACTCTGTTTAGTTGACAGG  
GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGACAGG  
GAAGTTTGGGATATACCCCAAAGTCTCTACCCCTCACTTTTATGGCCCTTTCCTAGATA  
TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTGATCAATA  
TATTGGAAATTAAAGTTTCTGACTTT

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## **FIGURE 242**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWFPASYPECGNNAQSPIDIQTDSVTFDPDLP
ALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKSGPGGSEHQ
INSEATFAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNRLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLL
FSTEEEPSKLLVQNYRALQPLNQRMVFAFSFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKSVVFTSAQATTEA
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

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**FIGURE 244**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM  
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE  
LPQIFTSLSLIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTTPAGRLPTPSG  
TDDDFAVTTTPAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16

**FIGURE 245**

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTCGGGCGGCCTCGGAGCGCGGCG  
GAGCCAGACGCTGACCACGTTCTCTCTCGGTCTCTCCGCCTCCAGCTCCGCGCTGCCCG  
GCAGCCGGGAGCC**ATG**CGACCCCAGGGCCCCGCCCTCCCCGAGCGGGCTCCGCGGCCTCC  
TGCTGCTCTGCTGCTGCAGCTGCCCCGCGCGTGCAGCGCCTCTGAGATCCCCAAGGGGAAG  
CAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG  
GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCATGTTATTCGGGTACACCTG  
GGATCCCAGGTCCGGGATGGATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAGCTTTGAG  
GAGTCCTGGACACCCAACCTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCT  
TGGGAAAATTGCGGAGTGACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT  
TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTC  
AATGGAGCTGAATGTTTCAGGACCTCTTCCATTGAAGCTATAATTTATTTGGACCAAGGAAG  
CCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGAAGGACTTTGTGAAG  
GAATTGGTGCTGGATTAGTGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAA  
GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAA**TA**  
**A**ATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAAT  
GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA  
CCAAAGTGTGATTTCACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAGT  
GGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA  
TAATTTGGAATATGTTGTGGTCTTTTGTTTTTCTCTTAGTATAGCATTTTTTAAAAAATA  
TAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTAAAT  
AAAAATTATTTCCAACA



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# FIGURE 246

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGGKQAQLRQREVVDLYNGMCLQGPA  
 PGRDGSPGANVIPGTPGIPGRDGFKEGKECLRESFEESWTPNYKQCSWSSLYGIDLGKIA  
 ECTFTKMRNSALRVLFSGLRLKCRNACCQRWYFTFNGAECGSLPIEAIYLDQGSPEMN  
 STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNVSRIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217